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OM protein - protein search, using sw model

Run on: May 2, 2002, 07:27:16 ; Search time 64.9 seconds

(without alignments)
216.018 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260
Sequence: 1 MGOCYKAGSGRTADDEGV.....LGFTRFLHGVTRGSRNTRR 623

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/6CTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------------|
| 1 | 3260 | 100.0 | 623 | 4 | US-09-347-801-4 |
| 2 | 2862 | 87.8 | 625 | 4 | US-09-347-801-18 |
| 3 | 1816.5 | 55.7 | 576 | 4 | US-09-347-801-19 |
| 4 | 883.5 | 27.1 | 639 | 4 | US-09-347-801-17 |
| 5 | 854 | 26.2 | 464 | 1 | US-07-951-715A-22 |
| 6 | 854 | 26.2 | 464 | 2 | US-08-459-448A-22 |
| 7 | 854 | 26.2 | 464 | 3 | US-08-459-595A-22 |
| 8 | 854 | 26.2 | 464 | 3 | US-08-459-504B-22 |
| 9 | 854 | 26.2 | 464 | 3 | US-08-459-444-22 |
| 10 | 817 | 25.1 | 463 | 1 | US-07-951-715A-25 |
| 11 | 817 | 25.1 | 463 | 2 | US-08-459-448A-25 |
| 12 | 817 | 25.1 | 463 | 3 | US-08-459-595A-25 |
| 13 | 817 | 25.1 | 463 | 3 | US-08-459-504B-25 |
| 14 | 817 | 25.1 | 463 | 3 | US-08-459-444-25 |
| 15 | 742 | 22.8 | 408 | 1 | US-07-951-715A-21 |
| 16 | 742 | 22.8 | 408 | 2 | US-08-459-448A-21 |
| 17 | 742 | 22.8 | 408 | 3 | US-08-459-595A-21 |
| 18 | 742 | 22.8 | 408 | 3 | US-08-459-504B-21 |
| 19 | 742 | 22.8 | 408 | 3 | US-08-459-444-21 |
| 20 | 548 | 16.8 | 456 | 1 | US-08-464-164-2 |
| 21 | 548 | 16.8 | 456 | 1 | US-08-338-057-2 |
| 22 | 548 | 16.8 | 456 | 2 | US-08-668-416-2 |
| 23 | 505.5 | 15.5 | 370 | 2 | US-08-878-989-19 |
| 24 | 505.5 | 15.5 | 370 | 2 | US-09-272-796-19 |
| 25 | 497 | 15.2 | 448 | 2 | US-09-159-385-2 |
| 26 | 497 | 15.2 | 448 | 4 | US-09-186-777-2 |
| 27 | 496.5 | 15.2 | 454 | 2 | US-09-159-385-1 |

| | | | | | | |
|----|-------|------|------|---|-------------------|--------------------|
| 28 | 496.5 | 15.2 | 454 | 4 | US-09-186-277-1 | Sequence 1, Appl1 |
| 29 | 486.5 | 14.9 | 424 | 2 | US-08-715-568A-1 | Sequence 1, Appl1 |
| 30 | 482.5 | 14.8 | 343 | 4 | US-08-878-989-5 | Sequence 5, Appl1 |
| 31 | 482.5 | 14.8 | 343 | 4 | US-09-272-796-5 | Sequence 5, Appl1 |
| 32 | 472 | 14.5 | 111 | 4 | US-09-347-801-8 | Sequence 8, Appl1 |
| 33 | 465 | 14.3 | 264 | 2 | US-07-857-224B-24 | Sequence 24, Appl1 |
| 34 | 457 | 14.0 | 157 | 4 | US-09-347-801-6 | Sequence 6, Appl1 |
| 35 | 453 | 13.9 | 1423 | 4 | US-08-810-712-10 | Sequence 10, Appl1 |
| 36 | 450 | 13.8 | 264 | 2 | US-07-857-224B-18 | Sequence 18, Appl1 |
| 37 | 449 | 13.8 | 331 | 4 | US-08-810-712-24 | Sequence 24, Appl1 |
| 38 | 444.5 | 13.6 | 387 | 1 | US-08-713-828-3 | Sequence 3, Appl1 |
| 39 | 444.5 | 13.6 | 387 | 2 | US-08-919-627-3 | Sequence 3, Appl1 |
| 40 | 444.5 | 13.6 | 387 | 2 | US-09-096-245-3 | Sequence 3, Appl1 |
| 41 | 444 | 13.6 | 264 | 2 | US-07-857-224B-19 | Sequence 19, Appl1 |
| 42 | 434.5 | 13.3 | 388 | 1 | US-08-713-828-5 | Sequence 5, Appl1 |
| 43 | 434.5 | 13.3 | 388 | 2 | US-08-919-627-5 | Sequence 5, Appl1 |
| 44 | 434.5 | 13.3 | 388 | 2 | US-09-096-245-5 | Sequence 5, Appl1 |
| 45 | 421.5 | 12.9 | 388 | 1 | US-08-713-828-4 | Sequence 4, Appl1 |

ALIGNMENTS

RESULT 1
US-09-347-801-4
; Sequence 4, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-347-801-4

Query Match 100.0%; Score 3260; DB 4; Length 623;

Best Local Similarity 100.0%; Pred. No. 3.8e-254; Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | MGOCYKAGSGRTADDEGVTEHQSPPPANGLPSTPRQQAQAQAVGTPRRRSGSKG | 60 |
| DB | 1 | MGOCYKAGSGRTADDEGVTEHQSPPPANGLPSTPRQQAQAQAVGTPRRRSGSKG | 60 |
| QY | 61 | STFGHQTPVAMPSPYPSGASPLPAGVSPSPARSTRPFRFPFPPSPAKHAKATLA | 120 |
| DB | 61 | STFGHQTPVAMPSPYPSGASPLPAGVSPSPARSTRPFRFPFPPSPAKHAKATLA | 120 |
| QY | 121 | KRLGGKKEETIPEEGVGAGGGGAADAEETPDKTFEFGSKNGAYELCKEYGR | 180 |
| DB | 121 | KRLGGKKEETIPEEGVGAGGGGAADAEETPDKTFEFGSKNGAYELCKEYGR | 180 |
| QY | 181 | GHFHTGSAAVVKKGKGYKQTAIVAKAKMTTASIEDVREVKILRALSGHNNLVKFEY | 240 |
| DB | 181 | GHFHTGSAAVVKKGKGYKQTAIVAKAKMTTASIEDVREVKILRALSGHNNLVKFEY | 240 |
| QY | 241 | DACEDGLNVIYVMECEGELLDRILANGKRYTEBDAIAIYVQIISVAFCHLQGVHRD | 300 |
| DB | 241 | DACEDGLNVIYVMECEGELLDRILANGKRYTEBDAIAIYVQIISVAFCHLQGVHRD | 300 |
| QY | 301 | LKPENFLTTDENAPMKLIDFGLSDFTRPDERLNDIGSAIYVAPEVLHRSYSMEADIW | 360 |
| DB | 301 | LKPENFLTTDENAPMKLIDFGLSDFTRPDERLNDIGSAIYVAPEVLHRSYSMEADIW | 360 |

QY 361 SIGVITVILLCGSRPFMAWTEGIFRSVLRADPNFDDSPMTVSAEKDFVKRLNDYR 420
DB 361 SIGVITVILLCGSRPFMAWTEGIFRSVLRADPNFDDSPMTVSAEKDFVKRLNDYR 420
QY 421 KRMVAVQALHPWLRDEQROIPDLILFRILKOYLATPPLKRLALKALSKALREDELLYL 480
DB 421 KRMVAVQALHPWLRDEQROIPDLILFRILKOYLATPPLKRLALKALSKALREDELLYL 480
QY 481 KLOFLEPRDGFVSLDNFRATLTRYLTDMKESRYLFEHLALEPLAYRMDEEECAAA 540
DB 481 KLOFLEPRDGFVSLDNFRATLTRYLTDMKESRYLFEHLALEPLAYRMDEEECAAA 540
QY 541 ISPVQLEALRMEELIAGTAFOQFEQGNRYISVEELAOELNLAPTHYSIVQDWIRKSDG 600
DB 541 ISPVQLEALRMEELIAGTAFOQFEQGNRYISVEELAOELNLAPTHYSIVQDWIRKSDG 600
QY 601 LNFLGFTKFLHGVITGINSNRRH 623
DB 601 LNFLGFTKFLHGVITGINSNRRH 623

RESULT 2
US-09-347-801-18
; Sequence 18, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-801-18

Query Match 87.8%; Score 2862; DB 4; Length 625;
Best Local Similarity 87.7%; Pred. No. 3, 9e-222;
Matches 561; Conservative 16; Mismatches 31; Indels 32; Gaps 7;
QY 1 MGOCYGR--GASGRT--ADDEGVVTEHOSPPRANGLPSTPRROQAQAQOVGTPRRR 55
DB 1 MGOCYGRAGASRHADHDADDSGASVAPSPPLRANGAPLP-----ATPRRH 47
QY 56 GSKSGSTTPGHQ---TPG--VAMPSPYSGASPLPAGVSPSPARSPRRFRFRPPPS 110
DB 48 --TSGSTTPVHNHQAATPRAAAMPSPYRAGASPLPAGVSPSPARSPRRFRFRPPPS 105
QY 111 PAKHIXATLAKKLGCGKPKAGTIPREBGVAGAGGGG-----GAADGAETERTLDKTCG 163
DB 106 PAKHIXATLAKKLGCGKPKAGTIPREBGVAGAGAGAGAGAAVGAADSDADRPDLKTCG 165
QY 164 FSNFNGAKYELGKVGNGHGTCSAVVKKGEYKQTVAVKTIARAKMTAISIEDVRE 223
DB 166 FAKNFGAKYDLGKVGNGHGTCSAVVKKGEYKQTVAVKTIARAKMTAISIEDVRE 225
QY 224 VKTLRLSGHNNLVKTYDACEGLNLYIWMELCEGELLDRILARGRYTEEDAKAIYVQ 283
DB 226 VKTLRLSGHNNLVKTYDACEGLNLYIWMELCEGELLDRILARGRYTEEDAKAIYVQ 285
QY 284 ILVAVFCHLQGVVHDLKPENFLFTTRDENAPKLLIDGLSDFTRPDERLNDIVGAYY 343
DB 286 ILVAVFCHLQGVVHDLKPENFLFTTRDENAPKLLIDGLSDFTRPDERLNDIVGAYY 345
QY 344 VAEVLRHSYSMEADWISIGVITVILLCGSRPFMAWTEGIFRSVLRADPNFDDSPMTV 403
DB 344 VAEVLRHSYSMEADWISIGVITVILLCGSRPFMAWTEGIFRSVLRADPNFDDSPMTV 403

DB 346 VAEVLRHSYSMEADWISIGVITVILLCGSRPFMAWTEGIFRSVLRADPNFDDSPMTV 405
QY 404 SAKAKDFVRLKNDYRKRMVAVQALHPWLRDEQROIPDLILFRILKOYLATPPLKRL 463
DB 406 SAKAKDFVRLKNDYRKRMVAVQALHPWLRDEQROIPDLILFRILKOYLATPPLKRL 465
QY 464 ALKALSKALREDELLYLKLOFLEPRDGFVSLDNFRATLTRYLTDMKESRYLFEHLAL 523
DB 466 ALKALSKALREDELLYLKLOFLEPRDGFVSLDNFRATLTRYLTDMKESRYLFEHLAL 525
QY 524 EPLAYRNDDEEECAAISPVQLEALRMEELIAGTAFOQFEQGNRYISVEELAOELNLA 583
DB 526 EPLAYRNDDEEECAAISPVQLEALRMEELIAGTAFOQFEQGNRYISVEELAOELNLA 585
QY 584 PTHYSIVQDWIRKSDGKLNFLGFTKFLHGVITGINSNRRH 623
DB 586 PTHYSIVQDWIRKSDGKLNFLGFTKFLHGVITGINSNRRH 625

RESULT 3
US-09-347-801-19
; Sequence 19, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-347-801-19

Query Match 55.7%; Score 1816.5; DB 4; Length 576;
Best Local Similarity 57.3%; Pred. No. 4, 3e-138;
Matches 358; Conservative 95; Mismatches 109; Indels 63; Gaps 9;
QY 1 MGOCYGRAGASRHADHDADDSGASVAPSPPLRANGLPSTPRROQAQAQOVGTPRRR 60
DB 1 MGOCYGRAGASRHADHDADDSGASVAPSPPLRANGLPSTPRROQAQAQOVGTPRRR 60
QY 61 STTPGHQTPGVAMPSPYSGASPLPAGVSPSPA-----RSPRRFRFRFRPPPSPAKH 115
DB 31 ---PRAKSGGFYSP-----SPYSLPKSPSVSSVSTPLRFRFRPPPSPAKH 81
QY 116 KATLAKRLGCGKPKAGTIPREBGVAGAGGGGGAADGAETERTLDKTCGSKNFGAKYELG 175
DB 82 KATLAKRLGCGKPKAGTIPREBGVAGAGGGGGAADGAETERTLDKTCGSKNFGAKYELG 175
QY 176 KEVGRGHGHTCSAVVKKGEYKQTVAVKTIARAKMTAISIEDVRRVQKTLRLSGHNN 235
DB 127 GEVGRGHGHTCSAVVKKGEYKQTVAVKTIARAKMTAISIEDVRRVQKTLRLSGHNN 235
QY 236 LKFTDACEGLNLYIWMELCEGELLDRILARGRYTEEDAKAIYVQILSVAVFCHLQ 295
DB 187 LKFTDACEGLNLYIWMELCEGELLDRILARGRYTEEDAKAIYVQILSVAVFCHLQ 295
QY 296 VVHDLKPENFLFTTRDENAPKLLIDGLSDFTRPDERLNDIVGAYYVAEVLHRSYSM 355
DB 247 VVHDLKPENFLFTTRDENAPKLLIDGLSDFTRPDERLNDIVGAYYVAEVLHRSYSM 355
QY 356 EADWISIGVITVILLCGSRPFMAWTEGIFRSVLRADPNFDDSPMTVSAEKDFVKRL 415
DB 307 EADWISIGVITVILLCGSRPFMAWTEGIFRSVLRADPNFDDSPMTVSAEKDFVKRL 415

| | | | |
|----|-----|---|-----|
| 0Y | 416 | NKDYRKRTAVQALTHPMU--RDDEOROLPDLILFRLLKQYLRAPTKRLKLSKRLRE | 474 |
| | | Y | |
| Db | 367 | NKDYRKRTLTAQAQALCHPWLGSHGELKTPSDMTIYKLVKTYIMSTLRSKSLAALAKTLIV | 426 |
| 0Y | 475 | DELLYLKIQKFLIEP-RDGEVSLDNFRTALTTRYLTDMAKESRYLEEFHALEPLAYRRMDP | 533 |
| | | | |
| Db | 427 | PQLAYLRQGFLLPDRSKNGYSMDNQNTAIIKSTSDAMKSDRPVDFHMIISCLQIKDF | 486 |
| 0Y | 534 | EEFCAAALSPQLALEERMEIAGTAQQOPEQBSNRIVSYVELAQELNLAPT--HHSIVQ | 591 |
| | | | |
| Db | 487 | EEFCASALSYVQLDAMETWEQHARRAYELEFEKDNRPRIETELASELGLTSVPVHVVLQ | 546 |
| 0Y | 592 | DWIRKSDGKLNFGFTKRIHQVTR- 616 | |
| | | | |
| Db | 547 | DWIRHSDGKLSFGFVRLHIGVSSR 571 | |

```

RESULT 4
US-09-347-801-17
: Patent 17, Application US/09347801
: Sequence No. 6262345
: GENERAL INFORMATION:
: APPLICANT: Allen, Steve
: APPLICANT: Lee, Jian Ming
: TITLE OF INVENTION: Plant Protein Kinases
: FILE REFERENCE: BB-1171
: CURRENT APPLICATION NUMBER: US/09/347,801
: CURRENT FILING DATE: 1999-07-02
: EARLIER APPLICATION NUMBER: 60/092,438
: EARLIER FILING DATE: July 10, 1998
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 17
: LENGTH: 639
: TYPE: PRT
: ORGANISM: Zea mays
: US-09-347-801-17

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| | | | | |
|-----------------------|-------------------|--------------------|------------|-------------|
| Query Match | 27.1%; | Score 883.5; | DB 4; | Length 639; |
| Best Local Similarity | 35.4%; | Pred. No. 5.4e-63; | | |
| Matches 219; | Conservative 102; | Mismatches 234; | Indels 63; | Gaps 17 |

| | | | |
|----|-----|--|-----|
| Qy | 25 | OSPRLANLETPRRQQAQAQAQVTPRRRSGSSGTPGHOHGVAMSPYPSDGSAP | 84 |
| Dd | 25 | KTPOEGDLP-----AANSPGGAGAGSOSALPKPASDVHNHVAOS-----EAP | 69 |
| Qy | 85 | LPAGVSPASRSTPRRFRKRPFRPPSPAKNIK-ATLAKRLGAG-----KPECTIPEEG | 137 |
| Dd | 70 | EPVKIAAHSEPAIVNREAPREPKIAASHSEPRAPMAKREGAANAANSPPSPRRPQVK | 129 |
| Qy | 138 | GVGAGGGGGAADAETERPDLKTFGFSKNEGAKYELGKEYGRGHG--HTCSAVYKGE | 195 |
| Dd | 130 | RVSASGILLGSVLRKTE-----NLKDXYSIGRLRGQGFCTHLC---VERA- | 174 |
| Qy | 196 | YKGQIVAAKIIAKAKMTAISIEDVRRREVKIARLSGHNILVYKYDCEGLNVIYMEI | 255 |
| Dd | 175 | -TGKELKASILKRLGDDDEVERREIQIHMHLIASHSPVVGIRGAYEDAVAAVHIMEL | 233 |
| Qy | 256 | CEGGLDLRILRAGRYEEDAKAIIVQIILSVAFCHLQGVNHDILPENLFTTREN | 315 |
| Dd | 234 | CGGGELEFRIYR-GHTYERKAALARYIVGVNACHSMGMHNDILPENLFDHSEEA | 292 |
| Qy | 316 | PMKLDFGLSOFIRPDERLNDIVSAYVAPEVLEHRSYMSIDFMSIGVITYIILCSRP | 375 |
| Dd | 293 | ALKTIDELSTIFFRRGQIFLTVDGSSPYVAPEVLEKRRGRPADVMSAGVIITYIILCGVP | 352 |
| Qy | 376 | FWARTESGIFRSVLRADENFDSPPTVASABAKDFVKRFLNKDYRKRMATAVALTHBWL | 435 |
| Dd | 353 | FWAENEGQIFEEVILHGRIDFSESPISDQAKDLVRMLVROBRKRLTAHEVLRHBMV- | 411 |
| Qy | 436 | DEQRQI-----PDILIFRLIKOYLRAIPLKRLALKAISKALREDBLLYKIQIQLLE | 488 |

Db 412 --- QVGVAVADRPDLSDAVLSVRMQLFSAMKMLKLMALRYAENLSDEDEINGLRMFKCID 467

QY 489 -PRGVEVSLDNFKRALTRYTLTDAMKESRVLEELHLEPLAYRRMDEEFCALAIPIQLE 547

Db 468 ADNSGQITFEELKVLKGLEVCVGN-LOESEIYALMKAADVNNGTIDYGEFTIATL---HLN 523

QY 548 ALEMEELAGTAPFOQFEGEGNRVLSVEL---AQLMLAPTH-SYIQWDIIRKSDGLNF 603

Db 524 KVER-EDHLPAFAFYFDKDGSGVITTADELAVACEFGISGVQLEDLIGVEDQDDNDGRIDY 582

QY 604 LGFTKFLHGVTIRGSNFR 621

Db 583 NEFYAMMKPITVGGSSRR 600

RESULT 5
 US-07-951-715A-22
 : Sequence 22, Application US/07951715A
 : Patent No. 5625136
 :
 : GENERAL INFORMATION:
 : APPLICANT: Kozziel, Michael G.
 : APPLICANT: Desai, Nallini M.
 : APPLICANT: Lewis, Kelly S.
 : APPLICANT: Kramer, Vance C.
 : APPLICANT: Warren, Gregory W.
 : APPLICANT: Evola, Stephen V.
 : APPLICANT: Crossland, Lyle D.
 : APPLICANT: Wright, Martha S.
 : APPLICANT: Merlitt, Ellis J.
 : APPLICANT: Launists, Karen L.
 : APPLICANT: Rothstein, Steven J.
 : APPLICANT: Bowman, Cindy G.
 : APPLICANT: Dawson, John L.
 : APPLICANT: Dunder, Erik M.
 : APPLICANT: Pace, Gary M.
 : APPLICANT: Suttle, Janet L.
 : TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 : TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 : NUMBER OF SEQUENCES: 94
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CIBA-GEIGY Corporation
 : STREET: 7 Skyline Drive
 : CITY: Hawthorne
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10532
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30B
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/07/951,715A
 : FILING DATE: 25-SEP-1992
 : CLASSIFICATION: 800
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/772,027
 : FILING DATE: 04-OCT-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Spruill, W. Murray
 : REGISTRATION NUMBER: 32,943
 : REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (919)541-8615
 : TELEFAX: (919)541-8689
 :
 : INFORMATION FOR SEQ ID NO: 22:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 464 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 :
 : HYPOTHETICAL: NO

FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note- "derived protein sequence of
OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-07-951-715A-22

Query Match 26.2% Score 854; DB 1; Length 464;
Best Local Similarity 40.0%; Pred. No. 8.2e-61;

Matches 186; Conservative 88; Mismatches 163; Indels 28; Gaps 10;

QY 156 RPLDKTFGSKNFGAKYELGKVGGRHFG--HTCSAVYKKGEGYQVAVYIAKAKMT 213
DB 4 RPE-----DVRATYSMGKELRGQGVTHLCT-----HRTSGEKLACKTIARKKLA 51
QY 214 AISIEDVREVKILRALSGHNNLVKFYDACEGLNVIYIMELCEGGLDRIILARGRYT 273
DB 52 REDVDVREVOQMHLHSGQPNVGLRGAYEDKQSVHLMELCAGGELFDRITAR-GQYT 110
QY 274 EEDAKAIVOILSVAFCHLQGVVHRDLKPENFLETTREDAVNAKMLIDPGLSDFIRPDR 333
DB 111 ERGAELRLAIYOIHTCHSMGVHRDIKPENFLLSKDEDAFLKATDFGLSVFKEGEL 170
QY 334 LNDIVGSAVYVAPVLRHSYMEADIMSGVITTYILLGSRPFWARTESGIFRSVLRADP 393
DB 171 LNDIVGSAVYVAPVLRHSYMEADIMSGVITTYILLGSRPFWARTESGIFRSVLRADP 393
QY 394 NEDDSPWPTVSAEAKDFVKRLNKKRMTAVOALTHFWLRD--EQQIPDLILIRLI 451
DB 231 DLSEPPHISPGAKDLVKMLINPKERLAFQVLNHPVKEGDDAPDPLDNVLDRL 290
QY 452 KOYLRTPLKRLALKSKALREDELLYKLOFLE--PRDGFVSLDNFRTALTALRYLTD 510
DB 291 KOFRAMNOFKKALRIITAGCLSEETITGLKEMFNIDKNSGTITDELKHLGAKH-GPK 349
QY 511 MKESVLEFLHALERPLAVRRMDFEEFCAAIAPYOLEALRMEIETAGTAFOQFDEGRV 570
DB 350 LSDSEMERKLEMAADADGNGLIDYDEFYATY--HMKKLDL-EEHLYTAFOYFDKNSGY 405
QY 571 ISVEL-----AOELNLAIPHYSIVODWIRKSDGKLNFLCFTKFL 610
DB 406 ITRKELEHALKEOGLYDADKIKIDISDSDSDNGRIDYSEFVAMM 450

RESULT 6
US-08-459-448A-22

Sequence 22, Application US/08459448A
Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Kozel, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Ewola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlino, Ellis J.
APPLICANT: Launus, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESSES:
ADDRESS: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005

CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note- "derived protein sequence of
OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-08-459-448A-22

Query Match 26.2% Score 854; DB 2; Length 464;
Best Local Similarity 40.0%; Pred. No. 8.2e-61;

Matches 186; Conservative 88; Mismatches 163; Indels 28; Gaps 10;

QY 156 RPLDKTFGSKNFGAKYELGKVGGRHFG--HTCSAVYKKGEGYQVAVYIAKAKMT 213
DB 4 RPE-----DVRATYSMGKELRGQGVTHLCT-----HRTSGEKLACKTIARKKLA 51
QY 214 AISIEDVREVKILRALSGHNNLVKFYDACEGLNVIYIMELCEGGLDRIILARGRYT 273
DB 52 REDVDVREVOQMHLHSGQPNVGLRGAYEDKQSVHLMELCAGGELFDRITAR-GQYT 110
QY 274 EEDAKAIVOILSVAFCHLQGVVHRDLKPENFLETTREDAVNAKMLIDPGLSDFIRPDR 333
DB 111 ERGAELRLAIYOIHTCHSMGVHRDIKPENFLLSKDEDAFLKATDFGLSVFKEGEL 170
QY 334 LNDIVGSAVYVAPVLRHSYMEADIMSGVITTYILLGSRPFWARTESGIFRSVLRADP 393
DB 171 LNDIVGSAVYVAPVLRHSYMEADIMSGVITTYILLGSRPFWARTESGIFRSVLRADP 393
QY 394 NEDDSPWPTVSAEAKDFVKRLNKKRMTAVOALTHFWLRD--EQQIPDLILIRLI 451
DB 231 DLSEPPHISPGAKDLVKMLINPKERLAFQVLNHPVKEGDDAPDPLDNVLDRL 290
QY 452 KOYLRTPLKRLALKSKALREDELLYKLOFLE--PRDGFVSLDNFRTALTALRYLTD 510
DB 291 KOFRAMNOFKKALRIITAGCLSEETITGLKEMFNIDKNSGTITDELKHLGAKH-GPK 349
QY 511 MKESVLEFLHALERPLAVRRMDFEEFCAAIAPYOLEALRMEIETAGTAFOQFDEGRV 570
DB 350 LSDSEMERKLEMAADADGNGLIDYDEFYATY--HMKKLDL-EEHLYTAFOYFDKNSGY 405


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8587
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION:
US-08-459-504B-22

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Query Match Best Local Similarity 26.28; Score 854; DB 3; Length 464; Pred. No. 8.2e-61;

Matches 186; Conservative 88; Mismatches 163; Indels 28; Gaps 10;

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QY 156 RPLDKTFGSKNFAGKYLKREKVGKRGHG--HTCSAVVKKGEYGVAVYKIIAKAMTT 213
DB 4 RPKM-----DVRATYSMGKELRGQGVYTHLCT-----HRTSGEKLACTTIKKRLAA 51
QY 214 AISEDVAREVKILRALSGHNNLVKFYDACEDEGLNVIYVMECEGGLDRIIARGGRYT 273
DB 52 REDVDVAREVOIHNHLSGQPNVVGKAYEDKQSVHLMELACGELFPRIIAR-GQYT 110
QY 274 EEDAKAIYVQILSVVARCHGVVHRLKPENFLFTTRDENAPMKLIDGELSPFIRDER 333
DB 111 ERGAELRLAIVOIVHTCHSMGVNHNDRKPENFLLSKDEDAFLKATDFGLVFFKEGEL 170
QY 334 LNDIVGSAVVYAEVLRHSYSMEADIMSIGVITYILLGSRPPMARTESGFSVSARAD 393
DB 171 LRDIIVGSAVYIAEVLKRYKGPREADIMSVMLYIFLAGVPPMAENENKIFAILRGOL 230
QY 394 NFDSDPMPYSAKAKDFVRFKLDYRKRRMTAVQALTHPWLRD--EQRQIPDLIDILFRLI 451
DB 231 DLSSEPPHISPAKDLVKMLINPKERLTAQVNLNHPWIKEDGADAPRTPLDNVVLDR 290
QY 452 KQYLRAIPLKRLKALSKALREDELLYLKLOKILLE-PRDGVSLDNRTALRLTLTA 510
DB 291 KQPRANNOFKKALRIIACLSSEETITGLKEMFNIDKNSGTTIYDELKHLAKH-GPK 349
QY 511 MKSRVLELLELHLEPLAYRMDFEFCAAIISPYOLEALERWEETAGTAFQOFQEGNRY 570
DB 350 LSSSESEKELMEADADGNGCLIDYDEVFATV---HNKIKDR-EBHLIYTAFOYFDKDNNGY 405
QY 571 ISVEEL-----AOELNLAPTHYSIVQDMTRKSDGKLNPLGFTKFL 610
DB 406 TKRELEHALKRGGLYDADKIDKIDISDADSDNDGRIDYSEFVAMM 450

```

RESULT 9
US-08-459-444-22
Sequence 0, Application US/08459444A
Patent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallas Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8587

SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Protein

LOCATION: 1..464

SEQUENCE DESCRIPTION: SEQ ID NO: 22

US-08-459-444-22

Query Match Best Local Similarity 26.28; Score 854; DB 3; Length 464; Pred. No. 8.2e-61;

Matches 186; Conservative 88; Mismatches 163; Indels 28; Gaps 10;

```

QY 156 RPLDKTFGSKNFAGKYLKREKVGKRGHG--HTCSAVVKKGEYGVAVYKIIAKAMTT 213
DB 4 RPKM-----DVRATYSMGKELRGQGVYTHLCT-----HRTSGEKLACTTIKKRLAA 51
QY 214 AISEDVAREVKILRALSGHNNLVKFYDACEDEGLNVIYVMECEGGLDRIIARGGRYT 273

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Db 52 REDVDYRRREVQIMHHISGQPNVVGELGAYEDKOSVHLVMEACGELFDRILAR-GQYT 110
QY 274 EDAKAIIVQILSVAFCHLQGVVHNDLKPENLFETTRDENAPMKLIDELSPFIRDER 333
Db 111 ERGAELRLAIVQIVHTCHSGVWMDIKPENLILSKDDADPKATSTDFPFKEGEL 170
QY 334 LNDIVSAYVAVPEVLRHSYSMEADWSIGVITYIILGSRPFWARTESGIFRSVLRADP 393
Db 171 LRIIVSAYVIAPEVLRKRKKGPEADIMSVGMVLIPLAGPPFWAEENEFITALLIGOL 230
QY 394 NPDSPWPVSAKDFVKFELKDKYRKRTAVQALTHPLRD--EORQIPDLILFRLI 451
Db 231 DLSEFPWPHISPAKDKLVKMLNINPERLTAFOVLNHPWIKEDGADPDTPLDNVLDRL 290
QY 452 KOYLRATPLKRLKALREDELLYLKLOKLE-PRDGFSVSDNFRATLRYLTDA 510
Db 291 KQIRANQKFAADRIITAGLSEELTGLEKEMFRNIDKNSGTTTDELHGLAKH-GPK 349
QY 511 MKSRVLEPLALEPLAIRMDFEEPCAAISPQYALERMEIAGTAFQOPEOEGNRV 570
Db 350 LSDSEMEKLEADADONGLIDYDEFATV---HMKKLDL-EEHLTATFOYFDKNSGY 405
QY 571 ISVEL-----AQLNAPTHYSIVQDMIRKSDGKLNFLGFTKFL 610
Db 406 ITRKELEHALKEOGLYDADKIKDIISDADSDNGRIDYSEFVAM 450

RESULT 10
US-07-951-715A-25
; Sequence 25, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rochstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; CLASSIFICATION: 800
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray

```

```

; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; OTHER INFORMATION: /note="protein sequence for
; OTHER INFORMATION: soybean CDPK as shown in figure 34."
US-07-951-715A-25

Query Match 25.1%; Score 817; DB 1; Length 463;
Best Local Similarity 38.9%; Pred. No. 7.7e-58;
Matches 178; Conservative 94; Mismatches 160; Indels 26; Gaps 11;

QY 165 SKNEGAKYELKEVGRGHFGHT--CSAVVKKGEKQGVAVKAIKAKMTAISIEDVRR 222
Db 6 TQNTREYVEYGRKKGQGFQFTFECTRRASGKR-----AKSIPKRLKCKEDYEDVWR 60
QY 223 EVKILRALSGHNNLVKYYDACEDGLNVIYMEICEGELLDRILARGRTTEDAKAIIV 282
Db 61 EIQIMHHISEHANVRIEGYVEDSTAVHLVMEICEGELDPRIYQK-GHYSERQARLIK 119
QY 283 QILSVAFCHLQGVVHNDLKPENLFETTRDENAPMKLIDGSLDFIRDERLNDIVSAY 342
Db 120 TTYEVVACHSLGVHMDLKPENLFETIDEDAKLATDFGLSYFYRGESFCDVVSPT 179
QY 343 YVAPPEVLRHSYSMEADWSIGVITYIILGSRPFWARTESGIFRSVLRADPNFDSWPT 402
Db 180 YVAPPEVLRKLYGPESDVMSAGVLIYILSGVPPWASESGIFQIILGKLDHFSEWPS 239
QY 403 VSAEAKDFVKFELKDKYRKRTAVQALTHPLRDQ--ROIPLDILFRLIKOYLRATPL 460
Db 240 ISDSAKDLIRKMDQNKTRTLTAHEVLRHPVLYDNDIAPPKPLDSAVLSRIKOPSANMK 299
QY 461 KRLAKLAKSALREDELLYLKLOKLE-PRDGFSVSDNFRATLRYLTPTAMKRSVLEF 519
Db 300 KKMALRYIAERLSEELTGLEKELFKMTIDTNSGTTTDELKDGKRVGSELM-ESETIKL 358
QY 520 LHALEPLAIRMDFEEPCAAISPQYALERMEIAGTAFQOPEOEGNRVIVSEELAQ- 578
Db 359 MDADIDKSGTIDYGEFTIATV---HMKLERENLV-SAFSYDKNGSGITTDELIOQA 414
QY 579 --EELNAPTHYSIVQDMIRK---SDGKLNFLGFTKFL 610
Db 415 CKDFGLDIDH---IDMIKEIDQNDQIDYGEFAAMM 449

RESULT 11
US-08-459-448A-25
; Sequence 25, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.

```

us-09-854-731-4.rai

```

1  APPLICANT: Rothstein, Steven J.
2  APPLICANT: Bowman, Cindy G.
3  APPLICANT: Dawson, John L.
4  APPLICANT: Dunder, Erik M.
5  APPLICANT: Pace, Gary M.
6  APPLICANT: Suttle, Janet L.
7  TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
8  TITLE OF SEQUENCES: INSECTICIDAL ACTIVITY IN MAIZE
9  NUMBER OF SEQUENCES: 94
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: No. 5859336artis Corporation
12 STREET: Patent 6 Trademark Dept., 520 White Plains
13 STREET: Rd., POB 2005
14 CITY: Tarrytown
15 STATE: New York
16 COUNTRY: USA
17 ZIP: 10591-9005
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: PatentIn Release #1.0, Version #1.30
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/08/459,448A
25 FILING DATE: 02-JUN-1995
26 CLASSIFICATION: 800
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/951,715
29 FILING DATE: 25-SEP-1992
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/772,027
32 FILING DATE: 04-OCT-1991
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Pace, Gary M.
35 REGISTRATION NUMBER: 40403
36 REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: (919)541-8582
39 TELEFAX: (919)541-8689
40 INFORMATION FOR SEQ ID NO: 25:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 463 amino acids
43 TYPE: amino acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: protein
47 HYPOTHEICAL: NO
48 FEATURE:
49 NAME/KEY: Protein
50 LOCATION: 1..463
51 OTHER INFORMATION: /note="protein sequence for
52 /S-08-459-448A-25 soybean CDPK as shown in Figure 34."

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| | | | | | |
|----|--|--------|--------------------|------------|-------------|
| | Query Match | 25.18; | Score 817; | DB 2; | Length 463; |
| | Best Local Similarity | 38.98; | Pred. No. 7.7e-58; | | |
| | Matches 178; Conservative | 94; | Mismatches 160; | Indels 26; | Gaps 11 |
| OY | 165 SKNGANGAYELGKEVGRGHFGHT--CSAVVKKEYKGQGVAVAKITIAKAKMTAISIEVVR | 222 | | | |
| Dd | 6 TONIREYVEYGRLLGGCGGFTTPECTRRASGKF-----ACKSLPKRKLCKEDEDYEYVMR | 60 | | | |
| OY | 223 EVKILRLSGHNHLYVFYDACEDEGLINVIYMELCEGSELDRIILARGRYTEEDAKAIVY | 282 | | | |
| Dd | 61 EIQLMHLSHANVAWVRIEGTYEDSPVAHVIMELCEGSELPRIYQK-GHSSEQAARLIK | 119 | | | |
| OY | 283 QIISVVAFCFLGDSVRODLKENPFLFTRDERNAAPMLIDGLSDFIIPDERLNDIVGSAY | 342 | | | |
| Dd | 120 TIYEVYLACHSCLGVMRDLKPENLFETIIDDAIKATIDGLSFYFKPGESFCDDVGSPY | 179 | | | |
| OY | 343 YVAPEVLHNSIKSMEDIWSIGVTITLLCGSRPMWATESGISFSVLRADPNPDSDSPPT | 402 | | | |

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Db      180  YVAPEVRLKRLGCEPSVWSAGVILLYLLSGVPFPAESEPFIROILLGKLDHFSEBWP 239
OY      403  VSAEADPEVKRFLNKKDYRRKMTAVOALTTHPMLRDEQ--ROJPLILFRLIKOYLRTPL 460
Db      240  IISDASDILIRKMLDQPKFTRLTAHEVLRHPMIVDNDLAPDPELDSAVLSRLKQFSAMNKL 299
OY      461  KRATALKSKALREDBLLYKLOFVLLP-PDQFVSLDNFRTALTRYLTDAMKESRYLEF 519
Db      300  KKALAVIERLSEEBIGGLKELFMIDTDSGTTTDELDKGLKRGSELM-ESEIKDL 358
OY      520  LHALEPLAVRMDPEFCAAAISPYOLEALRMEIEIAGTAFOOPEOGNIVISVEELAQ 578
Db      359  MDADADIKSGTIDYGEETAAATV---HLNKKLERENLV-SAFSVFDDKDGSGYITLDEIQQA 414
OY      579  --ELNAPHYISIVODWIRK-----SDGLNLTGTRKL 610
Db      415  CKDFGLDIDH---IDDMKTELQDNDGQIDIGFEPAAM 449

RESULT 12
US-08-459-595A-25
/ Sequence 25, Application US/08459595A
/ Patent No. 6018104
/ GENERAL INFORMATION:
/ APPLICANT: Kozziel, Michael G.
/ APPLICANT: Desai, Nalin M.
/ APPLICANT: Lewis, Kelly S.
/ APPLICANT: Kramer, Vance C.
/ APPLICANT: Warren, Gregory W.
/ APPLICANT: Evoila, Stephen V.
/ APPLICANT: Crossland, Lytle D.
/ APPLICANT: Wright, Martha S.
/ APPLICANT: Merlin, Ellis J.
/ APPLICANT: Launis, Karen L.
/ APPLICANT: Rothstein, Steven J.
/ APPLICANT: Bowman, Cindy G.
/ APPLICANT: Dawson, John L.
/ APPLICANT: Dunder, Erik M.
/ APPLICANT: Pace, Gary M.
/ APPLICANT: Suttler, Janet L.
/ TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
/ NUMBER OF INVENTIONS: INSECTICIDAL ACTIVITY IN MAIZE
/ NUMBER OF SEQUENCES: 94
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: No. 6018104artis Corporation
/ STREET: Patent & Trademark Dept., 520 White Plains
/ STREET: Rd., POB 2005
/ CITY: Tarrytown
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10591-9005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/459,595A
/ FILING DATE: 02-JUN-1995
/ CLASSIFICATION: 800
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 07/951,715
/ FILING DATE: 25-SEP-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/772,027
/ FILING DATE: 04-OCT-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pace, Gary M.
/ REGISTRATION NUMBER: 40403
/ REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (919)541-8582
/ TELEFAX: (919)541-8689

```

```

: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 463 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: MOLECULE TYPE: linear
: HYPOTHEICAL: NO
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..463
: OTHER INFORMATION: /note- "protein sequence for
: soybean CDPK as shown in figure 34."
US-08-459-595A-25

```

```

Query Match          25.1%; Score 817; DB 3; Length 463;
Best Local Similarity 38.9%; Pred. No. 7.7e-58;
Matches 178; Conservative 94; Mismatches 160; Indels 26; Gaps 11;

```

```

QY 165 SKNGAKYELKEVGRGHFGHT--CSAVVKKGEYKGTAVAKIITAKMTAISIEDVRR 222
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 TQNTREYVEVGRKLGQGGFGTTFECTRRASGKF-----ACKSTPKRLLCKEDIEDVWR 60
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 223 EVKILRALSGHNNLVKRYDAGEDGLNVIYVMECEGGLDRIILARGRYTEEDAKALIV 282
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 EIQIMHNLSEHANVRIEGTYEDSTAVHLVMECEGGLDRIIVYOK-CHYSEROAARLIK 119
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 283 QILSVAFCHQGVVHNDLKPENFLFTTRDENAPMKLIDFGLSPFIRDEBLNDIVGSAV 342
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 120 TIVEVEVCHSLGVVHNRDLKPENFLFTIDDAKIKATDFGLSVFYKGESFCVVGSPY 179
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 343 YVAEVLRHSYSMDADISIGVITYILLGSRPFWARTESGIFSVLRADNFDSPPT 402
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 180 YVAEVLRKLYGSPSDVWSAGVILYILSGVPPFAESPEPIFOIILGKIDFSEPPPS 239
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 403 VSAEAKDFVKRFLKDYRRKMTAVQALTHPWLDEQ--ROIPLDILFRLIKOYLRAATPL 460
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 240 ISDSAKDLIRKMLDQNPRTLRLLHAEVLRHPWIVDDNINAPKPLDSAVLSRLKQPSAMKL 299
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 461 KRLMLKSLKRLREDELLYLKLOKLE-PRDGFVSLDNFTALTRYLTIDAKESRVLEF 519
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 300 KKMALRYIAERLSEEGIGKLELFRKMTIDTNSGTTPELDLGDGRVSEELM-ESEIKDL 358
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 520 LHALEPLAYRRMDEFEFCALISPYOLEALRWEIAGTAQFQFQEGENRIVISVEELAO- 578
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 359 MDADIDKSGTIDYGERFLAATV---HLNKLREENVLV-SAFSYFDKDSGTYITIDEIOQA 414
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 579 --ELNLAPTHYSIVQDWIRK---SDGKLNFLGFTKFL 610
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 415 CKDFGLDDIH---IDDMIKELIDQNDQIDYGEFAAMM 449
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

```

RESULT 13
US-08-459-504B-25
: Sequence 25, Application US/08459504B
: Patent No. 6075185
: GENERAL INFORMATION:
: APPLICANT: Kozziel, Michael G.
: APPLICANT: Desai, Nalini M.
: APPLICANT: Lewis, Kelly S.
: APPLICANT: Kramer, Vance C.
: APPLICANT: Warren, Gregory W.
: APPLICANT: Eviola, Stephen V.
: APPLICANT: Crossland, Lyle D.
: APPLICANT: Wright, Martha S.
: APPLICANT: Merlin, Ellis J.
: APPLICANT: Launis, Karen L.
: APPLICANT: Rothstein, Steven J.
: APPLICANT: Bowman, Cindy G.
: APPLICANT: Dawson, John L.
: APPLICANT: Dunder, Erik M.
: APPLICANT: Pace, Gary M.

```

```

: APPLICANT: Suttie, Janet L.
: TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
: TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6075185artis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/459,504B
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/459,595
: FILING DATE: 02-JUN-1995
: APPLICATION NUMBER: US 07/951,715
: FILING DATE: 25-SEP-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/772,027
: FILING DATE: 04-OCT-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8587
: TELEFAX: (919)541-8689
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 463 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: MOLECULE TYPE: linear
: HYPOTHEICAL: NO
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..463
: OTHER INFORMATION: /note- "protein sequence for
: soybean CDPK as shown in figure 34."
US-08-459-504B-25

```

```

Query Match          25.1%; Score 817; DB 3; Length 463;
Best Local Similarity 38.9%; Pred. No. 7.7e-58;
Matches 178; Conservative 94; Mismatches 160; Indels 26; Gaps 11;
QY 165 SKNGAKYELKEVGRGHFGHT--CSAVVKKGEYKGTAVAKIITAKMTAISIEDVRR 222
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 TQNTREYVEVGRKLGQGGFGTTFECTRRASGKF-----ACKSTPKRLLCKEDIEDVWR 60
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 223 EVKILRALSGHNNLVKRYDAGEDGLNVIYVMECEGGLDRIILARGRYTEEDAKALIV 282
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 61 EIQIMHNLSEHANVRIEGTYEDSTAVHLVMECEGGLDRIIVYOK-CHYSEROAARLIK 119
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 283 QILSVAFCHQGVVHNDLKPENFLFTTRDENAPMKLIDFGLSPFIRDEBLNDIVGSAV 342
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 120 TIVEVEVCHSLGVVHNRDLKPENFLFTIDDAKIKATDFGLSVFYKGESFCVVGSPY 179
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 343 YVAEVLRHSYSMDADISIGVITYILLGSRPFWARTESGIFSVLRADNFDSPPT 402
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 180 YVAEVLRKLYGSPSDVWSAGVILYILSGVPPFAESPEPIFOIILGKIDFSEPPPS 239
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 403 VSAEAKDFVKRFLKDYRRKMTAVQALTHPWLDEQ--ROIPLDILFRLIKOYLRAATPL 460
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Db 240 ISDSAKLIRKMDONKRTLTAEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKL 299
QY 461 KRLAKLAKSALREDELLYLKLFKLE-PRDFVSLDNRTALTTRYLDAMKESRYLEF 519
Db 300 KKMALRYAERLSEELGKLEFKMIDTNSGTTTFDELKDLKRGVSELM-ESKIKDL 358
QY 520 LHALEPLAYRMDPEEFCAAIISPYOLEALERWEETAGTAFQOEQEGNRSIVSELAQ- 578
Db 359 MDADIDKSGTIDYGEFIATV---HLNKLREENLV-SAFSYFDKDGSGYITLDEIQQA 414
QY 579 --ELNLAPTHYSIVODIRK---SDGKLNFLGFTKFL 610
Db 415 CKDFGLDDIH---IDMWIKETIDQDNDQIDYGEFAAM 449

RESULT 14
US-08-459-444-25
; Sequence 0, Application US/08459444A
; Patent No. 6121014

GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

CORRESPONDENCE ADDRESS: 94
ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-Sep-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-Oct-1991

ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8587

TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: /note- "protein sequence for
soybean CDPK as shown in Figure 34."

SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-459-444-25

Query Match 25.1%; Score 817; DR 3; Length 463;
Best Local Similarity 38.9%; Pred. No. 7.7e-58;
Matches 178; Conservative 94; Mismatches 160; Indels 26; Gaps 11;

QY 165 SKNGAKYELGKGVGRGHGHT--CSAVVKKGEYKQTVAVKIKAKMTAISIEDVRR 222
Db 6 TONIREVEYVGKRLGOGFGTTPECTRASGKF-----AKSLPKRLCKEYEDVWR 60
QY 223 EYKILRASNNHNVKFPDACEDELNVYVLECEGELDRILKRGRTVEDAKAIV 282
Db 61 ELOIWHLSERHANVRIEGTYEDSTAVHLVMECEGELFDRIOK-GHYSERQAAHLK 119
QY 283 QILSVAFCHLQGVNRDLKPFENLFETTRDNAPMKLIDFGLDFIRPDELDNIYGSAY 342
Db 120 TIVEVVEACHSLGVNHRDLKPFENLFOTIDEDAKLKTDFGLSVFYKPGESFCVGVSPY 179
QY 343 YVAPVLRHRSYMEADWSIGVITYILLGSRPFWARTESGIFRSVLRADPNFDSFMPY 402
Db 180 YVAPVLRHRSYMEADWSIGVITYILLGSRPFWARTESGIFRSVLRADPNFDSFMPY 239
QY 403 VSAEAKDFVKRFLNKQYRKMTAVQALTHPMLRDEQ--RQIPDLIFRLIKQYLRATPL 460
Db 240 ISDSAKLIRKMDONKRTLTAEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKL 299
QY 461 KRLAKLAKSALREDELLYLKLFKLE-PRDFVSLDNRTALTTRYLDAMKESRYLEF 519
Db 300 KKMALRYAERLSEELGKLEFKMIDTNSGTTTFDELKDLKRGVSELM-ESKIKDL 358
QY 520 LHALEPLAYRMDPEEFCAAIISPYOLEALERWEETAGTAFQOEQEGNRSIVSELAQ- 578
Db 359 MDADIDKSGTIDYGEFIATV---HLNKLREENLV-SAFSYFDKDGSGYITLDEIQQA 414
QY 579 --ELNLAPTHYSIVODIRK---SDGKLNFLGFTKFL 610
Db 415 CKDFGLDDIH---IDMWIKETIDQDNDQIDYGEFAAM 449

RESULT 15
US-07-951-715A-21
; Sequence 21, Application US/07951715A
; Patent No. 5625136

GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Applicant: Dunder, Erik M.
Applicant: Pace, Gary M.
Applicant: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESS: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-951-715A-21

Query Match 22.8%; Score 742; DB 1; Length 408;

Best Local Similarity 40.4%; Pred. No. 7e-52; Matches 159; Conservative 77; Mismatches 144; Indels 14; Gaps 7;

QY 225 KILRALSGNNLVKFEYDACEGLNVIYIMELCEGGLDRIILARGRYTEEDAKAIYVOI 284
DB 1 QIMHLSGQPRVVGIRGAYEDKQSHVLMELCAGGLDFRIIAR-GYTERGAELLRAI 59
QY 285 LSVYAFCHLOGVHBDLKPENFLFTTRDENAPMKLIDFGLSDFIRPDERLNDIVGSAYYV 344
DB 60 VOIYHTCSMGVMHRDIPENFLLSKDEDAPLKATDFGLSVFEKGLRLDIVGSAYYI 119
QY 345 APEYLHRSYMEADISWISGVTYIILGSRPFMARTESGIFRSVLRADPNFDDSPMPTVS 404
DB 120 APEVLKRYGPEADISWISGVTYIILGSRPFMARTESGIFRSVLRADPNFDDSPMPTVS 179
QY 405 AEAKDFVRFLNKDYRKRMATVQALTHPLRD--EORQIPDLILIFRLIKOYLRAIPLKR 462
DB 180 PGARDLVKKMLNINPKERLTAFQVNLNHPWIKEDGAPPTPLDNVLDRLKQFRANQFKK 239
QY 463 LALKALSKALREDELLYLKLPKLE-PRDGFVSIDNFRALTTRYLTDAMKESRVLEFLH 521
DB 240 AALRIIACLSSEETITGKEMFKNIDKNSGTTITLDELKHGLAKH-GPKLSDSEMEKIME 298
QY 522 ALEPLAYRRMFEEFCAAIISPYOLEALERMWEIAGTAFQOFEQGNRVISVEEL----- 576
DB 239 AADADGNGLIIDFVATV--HNNKLDR-BEHILYTAFOYFDKNSGTTITKELEHALK 354
QY 577 AQELNLAPTHYSIVQDWIRKSDGKLNLFGLFTKFL 610
DB 355 EGGLEYDADKIKDIISDADSDNDGRIDYSEFVAMM 388

Search completed: May 2, 2002, 08:40:19
Job time: 4383 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2002, 06:25:16 ; Search time 71.49 Seconds
(without alignments)

663.824 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260

Sequence: 1 MGOCYKAGKASGRTADDEGV.....LGFYKFLHGVIRGSRTRH 623

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pirl:*\n2: pirl:*\n3: pirl:*\n4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 2862 | 87.8 | 625 | 2 T02033 | calcium/calmodulin |
| 2 | 2831 | 86.8 | 607 | 2 T03023 | calcium-dependent |
| 3 | 2179 | 66.8 | 595 | 2 B84906 | probable calcium-d |
| 4 | 1970 | 60.4 | 594 | 2 T45842 | calcium dependent |
| 5 | 1917 | 58.8 | 601 | 2 T46084 | CDPK-related prote |
| 6 | 1894 | 58.1 | 602 | 2 S60052 | calcium-dependent |
| 7 | 1829 | 56.1 | 577 | 2 T51264 | calcium-dependent |
| 8 | 1816.5 | 55.7 | 576 | 2 T02105 | calcium-dependent |
| 9 | 1760.5 | 54.0 | 606 | 2 D96532 | probable CDPK-rela |
| 10 | 1153.5 | 35.4 | 571 | 2 T00835 | calcium-dependent |
| 11 | 1080 | 33.1 | 536 | 2 T05500 | calcium-dependent |
| 12 | 923.5 | 28.3 | 583 | 2 H84810 | probable calcium-d |
| 13 | 904.5 | 27.7 | 533 | 1 S56552 | calcium-dependent |
| 14 | 903.5 | 27.7 | 529 | 1 S71774 | calcium-dependent |
| 15 | 895.5 | 27.5 | 573 | 2 T09940 | calcium-dependent |
| 16 | 889.5 | 27.3 | 540 | 1 T01889 | calcium-dependent |
| 17 | 886 | 27.2 | 531 | 1 T02993 | calcium-dependent |
| 18 | 886 | 27.2 | 554 | 1 T05476 | calcium-dependent |
| 19 | 883.5 | 27.1 | 639 | 1 T02784 | calcium-dependent |
| 20 | 877 | 26.9 | 610 | 1 A49082 | calcium-dependent |
| 21 | 865 | 26.5 | 513 | 1 T02259 | calcium-dependent |
| 22 | 860 | 26.4 | 554 | 1 T03263 | calcium-dependent |
| 23 | 859.5 | 26.4 | 531 | 2 D85059 | probable calcium d |
| 24 | 854 | 26.2 | 490 | 1 S71776 | calcium-dependent |
| 25 | 853.5 | 26.2 | 465 | 1 T03024 | calcium-dependent |
| 26 | 852.5 | 26.2 | 465 | 1 T46189 | calcium-dependent |
| 27 | 848.5 | 26.0 | 553 | 1 T02139 | calcium-dependent |
| 28 | 847.5 | 26.0 | 532 | 2 T14335 | protein kinase, ca |
| 29 | 843.5 | 25.9 | 492 | 1 T03271 | calcium-dependent |

| | | | | | |
|----|-------|------|-----|----------|---------------------|
| 30 | 843.5 | 25.9 | 514 | 2 T10938 | calcium-dependent |
| 31 | 841.5 | 25.8 | 521 | 2 G96543 | calcium-dependent |
| 32 | 838 | 25.7 | 493 | 1 S46283 | calcium-dependent |
| 33 | 837.5 | 25.7 | 541 | 2 F96776 | hypothetical prote |
| 34 | 835 | 25.6 | 545 | 2 H86322 | calcium-dependent |
| 35 | 834 | 25.6 | 503 | 2 T51156 | calcium-dependent |
| 36 | 832 | 25.5 | 495 | 2 T08874 | calcium-dependent |
| 37 | 829 | 25.4 | 455 | 1 S46284 | calcium-dependent |
| 38 | 828.5 | 25.4 | 533 | 1 S71778 | calcium-dependent |
| 39 | 824.5 | 25.3 | 501 | 2 G85097 | hypothetical prote |
| 40 | 821 | 25.2 | 520 | 2 F85059 | probable calcium d |
| 41 | 820.5 | 25.2 | 582 | 2 E84721 | probable calcium-d |
| 42 | 819.5 | 25.1 | 487 | 1 S71770 | calcium-dependent |
| 43 | 817 | 25.1 | 508 | 1 A43713 | calcium-dependent |
| 44 | 816.5 | 25.0 | 556 | 2 T06126 | calcium-dependent |
| 45 | 811 | 24.9 | 544 | 2 D84550 | probable calmodulin |

ALIGNMENTS

RESULT 1

calcium/calmodulin-dependent protein kinase homolog - maize

C/Species: Zea mays (maize)

C/Date: 26-Feb-1999 #sequence-revision 26-Feb-1999 #text-change 17-Nov-2000

C/Accession: T02033; T02994; T01694

R/Lu, Y.T.; Hidaka, H.; Feldman, L.J.

Planta 199, 18-24, 1996

A/Title: Characterization of a calcium/calmodulin-dependent protein kinase homolog fr

A/Reference number: Z14504; MUID:96236830

A/Accession: T02033

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-625 <LUY>

A/Cross-references: EMBL:S82324; NID:g1839596; PIDN:AA647181.1; PID:g1839597

A/Experimental source: CV, Merit

R/Furumoto, T.; Ogawa, N.; Hata, S.; Izui, K.

FEBS Lett. 396, 147-151, 1996

A/Title: Plant calcium-dependent protein kinase-related kinases (CRK) do not require

A/Reference number: Z14398; MUID:97072168

A/Accession: T02994

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 29-146, 'GA', 147-625 <FUR>

A/Cross-references: EMBL:D84507; NID:g1313906; PIDN:BA12691.1; PID:g1313907

A/Experimental source: Strain Inbred line H84; root

A/Accession: T01694

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 174-398, 'G', 400-625 <FUR>

A/Cross-references: EMBL:D38452; NID:g2443387; PIDN:BA22410.1; PID:g2443388

A/Experimental source: leaf

C/Genetics:

C/Suprafamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

F:172-436/Domain: protein kinase homology <KIN>

Query Match 87.8%; Score 2862; DB 2; Length 625;

Best Local Similarity 87.7%; Pred. No. 7.7e-102;

Matches 561; Conservative 16; Mismatches 31; Indels 32; Gaps 7;

| | | | |
|----|-----|---|-----|
| QY | 1 | MGOCYK--GASGR---ADDEGGVTEHOSPPRNGLPSTPRPQQAQAQAQOQVTPRR | 55 |
| DB | 1 | MGOCYKAGKASRRADHDADPSGASVAPSPPLRANGAPLP-----ATPRKH | 47 |
| QY | 56 | GSKSGSTTPGHQ---TPG-VAMPSPYPSGASPLPAGVSPSPARSTRRFRFPFPPS | 110 |
| DB | 48 | --KSGSTPRVHHQAAATGGAAMPSPYPAGASPLPACVSPSPARSTRRFRFPFPPS | 105 |
| QY | 111 | PAKHATLARKLGGKKEGTTPREGVAGGGG-----GAADAETRPDKTFG | 163 |

Db 106 PAKHAKATLAKRLGGCKRKEGTIPBEGGACAGAGAGACAAGAAVGAADSAEDRPLKLTG 165

OY 164 FSKNEGKAYELGKVEYGVGHGHCASAVVKKGEYKGTVAVKITAKAKMTAISIEDVRE 223

Db 166 PAKFEGAKYDLGKVEYGVGHGHCASAVVKKGEYKGTVAVKITAKAKMTAISIEDVRE 225

OY 224 VKILRALSGHNNVVKFEDACEDGLNYYIWMELCEGELLDRILARGRYTEEDAKAIYVQ 283

Db 226 VKILKALSGHNNVVKFEDACEDGLNYYIWMELCEGELLDRILARGRYTEEDAKAIYVQ 285

OY 284 ILSVAVFCHLQGVYHNDLKPENFLFTTRDENAPMKLIDGLSDPIRPERLNDIVGSAVY 343

Db 286 ILSVAVFCHLQGVYHNDLKPENFLFTTRDENAPMKLIDGLSDPIRPERLNDIVGSAVY 345

OY 344 VAREVHRSTYSMEADIMSGVITYILLGSRPFWARTESGIFRSVLRADPNFDDSPWPSV 403

Db 346 VAREVHRSTYSMEADIMSGVITYILLGSRPFWARTESGIFRSVLRADPNFDDSPWPSV 405

OY 404 SAKAFQVVRFLNKDYRKRMATAVQALTHPMLRDEORQIPDLILFRILKQYLKATPLKRL 463

Db 406 SAKAFQVVRFLNKDYRKRMATAVQALTHPMLRDEORQIPDLILFRILKQYLKATPLKRL 465

OY 464 ALKALSKALREDELVLKLOFKLLEPRROGFSVLDNFRALTRYLDAMKESVLEFLHAL 523

Db 466 ALKALSKALSEDELVLKLOFKLLEPRROGFSVLDNFRALTRYLDAMKESVLEFLHAL 525

OY 524 EPLAVRRMDFEEFCAAAISPYOLEALEREWEIAGTAFQOEQEGNRIVSVEELAOELNLA 583

Db 526 EPLAVRRMDFEEFCAAAISPYOLEALEREWEIAGTAFQOEQEGNRIVSVEELAOELNLA 585

OY 584 PTHYSIVQMIKSDGKLNFLGFTFKFLHGVTIRGSNTRRH 623

Db 586 PTHYSIVQMIKSDGKLNFLGFTFKFLHGVTIRGSNTRRH 625

RESULT 2

703023
calcium-dependent protein kinase-related protein kinase - maize
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03023
R:Furumoto, T.; Ogawa, N.; Hate, S.; Izui, K.
FEBS Lett. 396, 147-151, 1996
A:Title: Plant calcium-dependent protein kinase-related kinases (CRK) do not require cal
A:Reference number: Z14398; MUID:97072168
A:Accession: T03023
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-607 <FUR>
A:Cross-references: EMBL:DB4508; NID:g1313908; PIDN:BAAL2692.1; PID:g1313909
A:Experimental source: strain inbred line H84; root
A:Note: does not require calcium for its activity
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
F:154-418/Domain: protein kinase homology <KIN>

Query Match 86.8%; Score 2831; DB 2; Length 607;
Best Local Similarity 88.3%; Pred. No. 1.1e-100;
Matches 553; Conservatve 18; Mismatches 33; Indels 22; Gaps 7;

OY 1 MGOCYGRK-GASGRADDEGGVTEHQSPPPANGLPSTPRQQAQAQAQVGTPRRRGSK 58

Db 1 MGOCYGAAGASRRADHDVAAP--PSPLPANGAP--TPQDPA-----TPGRR--K 47

OY 59 SGSTTP-GHQTGVAVMSPYPSGASPLPAGVSPSPARSTPRFRFRPPPPPAKHAK 117

Db 48 SGSTTPVNHQAATTAWSPYRAGASPLPAGVSPSPARSTPRFRFRPPPPPAKHAK 107

OY 118 TLAKRLGGCKRKEGTIPBEGGACAGAGAGACAAGAAVGAADSAEDRPLKLTGFSKAKYELGKE 177

Db 108 TLAKRLGGCKRKEGTIPBEGGACV-----AADSAEDRPLDKTGFANNGAKYDLGKE 161

OY 178 VGRGHGHTCSAVVKKGEYKGTVAVKITAKAKMTAISIEDVREVKILRALSGHNNLV 237

Db 162 VGRGHGHTCSALVKKGEYKGNAAVAKITAKAKMTAISIEDVREVKILRALSGHNNLV 221

OY 238 KRYDACEDGLNYYIWMELCEGELLDRILARGRYTEEDAKAIYVQILSVAFCHLQGV 297

Db 222 KRYDACEDGLNYYIWMELCEGELLDRILARGRYTEEDAKAIYVQILSVAFCHLQGV 281

OY 298 HRDLKPENFLFTTRDENAPMKLIDGLSDPIRPERLNDIVGSAVYVAREVHRSTYSME 357

Db 282 HRDLKPENFLFTTRDENAPMKLIDGLSDPIRPERLNDIVGSAVYVAREVHRSTYSME 341

OY 358 DIWSIGVITYILLGSRPFWARTESGIFRSVLRADPNFDDSPWPSVSAEAKDFPKRLNK 417

Db 342 DIWSIGVITYILLGSRPFWARTESGIFRSVLRADPNFDDSPWPSVSAEAKDFPKRLNK 401

OY 418 DYRRMPTAVQALTHPMLRDEORQIPDLILFRILKQYLKATPLKRLKALSKALREDEL 477

Db 402 DYRRMPTAVQALTHPMLRDEORQIPDLILFRILKQYLKATPLKRLKALSKALREDEL 461

OY 478 LYKLOFKLLEPRROGFSVLDNFRALTRYLDAMKESVLEFLHALPPLAVRRMDFEEFC 537

Db 462 LYKLOFKLLEPRROGFSVLDNFRALTRYLDAMKESVLEFLHALPPLAVRRMDFEEFC 521

OY 538 AAASIPYOLEALEREWEIAGTAFQOEQEGNRIVSVEELAOELNLAFTHYSIVQMIKRS 597

Db 522 AAASIPYOLEALEREWEIAGTAFQOEQEGNRIVSVEELAOELNLAFTHYSIVQMIKRS 581

OY 598 DGKLNFLGFTFKFLHGVTIRGSNTRRH 623

Db 582 DGKLNFLGFTFKFLHGVTIRGSNTRRH 607

RESULT 3

B84906
probable calcium-dependent protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: B84906
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
J.; Guss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: B84906
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-595 <STO>
A:Cross-references: GB:AE002093; NID:g3831444; PIDN:AC69927.1; GSPDB:GN00139
A:Genetics:
A:Gene: At2g46700
A:Map position: 2

Query Match 66.8%; Score 2179; DB 2; Length 595;
Best Local Similarity 68.3%; Pred. No. 4.8e-76;
Matches 426; Conservatve 71; Mismatches 93; Indels 34; Gaps 7;

OY 1 MGOCYGRK-GASGRADDEGGVTEHQSPPPANGLPSTPRQQAQAQAQVGTPRRRGSKS 59

Db 1 MGOCYGVKQSKONGEENATTTYYVSGDNGIQPLTP-----VWGKAKNTPA 49

OY 60 GSTPFGHQTGVAVMSPYPSGASPLPAGVSPSPAR-STPRFRFRPPPPPAKHAKAT 118

Db 50 RSSNPS-----PWSPPPHGASAPLPAGVSPSPARSTPRFRFRPPPPPAKHAKAS 103

OY 119 LAKRLGGCKRKEGTIPBEGGACAGAGAGACAAGAAVGAADSAEDRPLKLTGFSKAKYELGKEV 178

Db 104 LAKRL-GVAKPRKGIPEE-----KGTPEPDSLKSGYGVKNGAKYELGKEV 149

OY 179 GRGHGHTCSAVVKKGEYKGTVAVKITAKAKMTAISIEDVREVKILRALSGHNNLVK 238

Db 179 GRGHGHTCSAVVKKGEYKGTVAVKITAKAKMTAISIEDVREVKILRALSGHNNLVK 238

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Db 150 GRGHFGTSCGRKKGDKIHPVAVKIIISKAKMTTAIEDVREVKLLSLSGHKYLIK 209
QY 239 FYDACEEDGLNVIYVMEICEGEGELDLRLILARGRYTEEDAKAIVQIISVAFCHLQGVH 298
Db 210 XYDACEEDANNVIYVMEICEGEGELDLRLILARGRYTEEDAKAIVQIISVAFCHLQGVH 269
QY 299 RDLKPEMFLETTREBNAPMKLIDFGLSDFIKPPDLNDIYGSATVYVAPEVYHRSYSMEAD 358
Db 270 RDLKPEMFLETTREBNAPMKLIDFGLSDFIKPPDLNDIYGSATVYVAPEVYHRSYSMEAD 329
QY 359 IMSIGVITVILCGSRPFMAATESGIFRSYVLRADPNFDDSPMPVSAEAKDFVRFLNKD 418
Db 330 IMSIGVITVILCGSRPFMAATESGIFRSYVLRADPNFDDSPMPVSAEAKDFVRFLNKD 389
QY 419 YRKRMATAVQALTHFWLDEORFOIPDLILIFRLIKOYLRAPEPLKRLAKALSKALREDELL 478
Db 390 YRKRMATAVQALTHFWLDEORFOIPDLILIFRLIKOYLRAPEPLKRLAKALSKALREDELL 449
QY 479 YLKIQFKLEP-RDGEVSLDNFRTALTRYLTDAMKESRYLEFLHALPELAYRMDPEEFC 537
Db 450 YLKIQFKLEP-RDGEVSLDNFRTALTRYLTDAMKESRYLEFLHALPELAYRMDPEEFC 509
QY 538 AAASPVQLEALEREWEIAGTAFOEBOGNRVISVEELAOELNAPTHYSIVODMIRKS 597
Db 510 AAASPVQLEALEREWEIAGTAFOEBOGNRVISVEELAOELNAPTHYSIVODMIRKS 569
QY 598 DGKLNFLGFTKFLHGVITRGSNTR 621
Db 570 DGKLNFLGFTKFLHGVITRGSNTR 593

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RESULT 4

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T45842
calcium dependent protein kinase-like - Arabidopsis thaliana
N:Alternate names: protein F2K15.230
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence: revision 04-Feb-2000 #text: change 04-Mar-2000
C:Accession: T45842
R:Rieger, M.; Gabel, C.; Mueller-Luer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223015
A:Accession: T45842
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-594 <RIE>
A:Cross-references: EMBL:AL132956
A:Experimental source: cultivar Columbia; BAC clone F2K15
C:Genetics:
A:Map position: 3
A:Introns: 180/3; 224/2; 238/2; 274/3; 301/1; 400/1; 436/3; 471/3; 492/3; 548/3
A>Note: F2K15.230
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold

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Query Match 60.4%; Score 1970; DB 2; Length 594;
Best Local Similarity 62.8%; Pred. No. 3.8e-68;
Matches 391; Conservative 81; Mismatches 117; Indels 34; Gaps 8;

QY 1 MGOCYVGKASGRTADDEGGVTEHQSPPANGLPSTPRQAOAOQVGTPRRGRSG 60
Db 1 MGHCYSKRISIVDDDE-----IPS-----ATAOPLRHSQNHQIYSSS 39
QY 61 STTPGHQTPGVAMPSPYR-SGASPLPAGVSPSPARSTPRRFRKRPFPSPAPAKHAKTL 119
Db 40 SSIP--QSPATSEVNPVNIISFPQSLPAGVAPSPAR-TPGKFKFMPFPFPSPAPAKHAKTL 96
QY 120 AKRLG-GGKPEEGTIPBEGVAGAGGGGGAADGATERPLDKTGFSGKNFCAYELGKEV 178
Db 97 RRRRGTAHPRPDGPIDPEDEAGSGGSGIG-----ER-LDKNFGFAKNFGCKYELGKEV 148
QY 179 GRGHFGHTCSGVVKKGEKGTAVAKIIAKAKMTTAISIEDVREVKLLSLSGHKYLIK 238
Db 149 GRGHFGHTCSGVVKKGEKGTAVAKIIAKAKMTTAISIEDVREVKLLSLSGHKYLIK 208

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QY 239 FYDACEEDGLNVIYVMEICEGEGELDLRLILARGRYTEEDAKAIVQIISVAFCHLQGVH 298
Db 209 FYDACEEDGLNVIYVMEICEGEGELDLRLILARGRYTEEDAKAIVQIISVAFCHLQGVH 268
QY 299 RDLKPEMFLETTREBNAPMKLIDFGLSDFIKPPDLNDIYGSATVYVAPEVYHRSYSMEAD 358
Db 269 RDLKPEMFLETTREBNAPMKLIDFGLSDFIKPPDLNDIYGSATVYVAPEVYHRSYSMEAD 328
QY 359 IMSIGVITVILCGSRPFMAATESGIFRSYVLRADPNFDDSPMPVSAEAKDFVRFLNKD 418
Db 329 IMSIGVITVILCGSRPFMAATESGIFRSYVLRADPNFDDSPMPVSAEAKDFVRFLNKD 388
QY 419 YRKRMATAVQALTHFWLDEORFOIPDLILIFRLIKOYLRAPEPLKRLAKALSKALREDELL 478
Db 389 YRKRMATAVQALTHFWLDEORFOIPDLILIFRLIKOYLRAPEPLKRLAKALSKALREDELL 448
QY 479 YLKIQFKLEP-RDGEVSLDNFRTALTRYLTDAMKESRYLEFLHALPELAYRMDPEEFC 538
Db 449 YLKIQFKLEP-RDGEVSLDNFRTALTRYLTDAMKESRYLEFLHALPELAYRMDPEEFC 508
QY 539 AAASPVQLEALEREWEIAGTAFOEBOGNRVISVEELAOELNAPTHYSIVODMIRKS 598
Db 509 AAASPVQLEALEREWEIAGTAFOEBOGNRVISVEELAOELNAPTHYSIVODMIRKS 568
QY 599 GKLNFLGFTKFLHGVITRGSNTR 621
Db 569 GKLNFLGFTKFLHGVITRGSNTR 591

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RESULT 5

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T46084
CDPK-related protein kinase - Arabidopsis thaliana
N:Alternate names: protein T20E23.130
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence: revision 04-Feb-2000 #text: change 04-Mar-2000
C:Accession: T46084
R:Barajas, M.; Perez-Perez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Mewes, H.W.;
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223020
A:Accession: T46084
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-601 <BAR>
A:Cross-references: EMBL:AL133363
A:Experimental source: cultivar Columbia; BAC clone T20E23
C:Genetics:
A:Map position: 3
A:Introns: 186/3; 230/2; 244/2; 280/3; 307/1; 406/1; 443/3; 479/3; 500/3; 556/3
A>Note: T20E23.130
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

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Query Match 58.8%; Score 1917; DB 2; Length 601;
Best Local Similarity 60.4%; Pred. No. 3.8e-66;
Matches 380; Conservative 87; Mismatches 116; Indels 46; Gaps 9;

QY 1 MGOCYVGKASGRTADDEGGVTEHQSPPANGLPST-----PPOAOAOAOQVGTPRRGRSG 56
Db 1 MGLCTSKPNSNS-----DOTPARNSPLRASEVYKSSSSVNGEDDCVTTNNEG 50
QY 57 SKSG-----STTPGHQTPGVAMPSPYRSGASPLPAGVSPSPARSTPRRFRKRPFPSP 111
Db 51 KSPFPFPYSPSPAHYFSPSKTTPARSPATNST-----NSTPRFRKRPFPSP 99
QY 112 AKHIAKATLAKRLGGCKPEEGTIPBEGVAGAGGGGGAADGATERPLDKTGFSGKNFCAY 171
Db 100 AKHIAKATLAKRLGGCKPEEGTIPBEGVAGAGGGGGAADGATERPLDKTGFSGKNFCAY 147
QY 172 YELGKEVGRGHFGHTCSGVVKKGEKGTAVAKIIAKAKMTTAISIEDVREVKLLSLSGHKY 231
Db 148 YELGKEVGRGHFGHTCSGVVKKGEKGTAVAKIIAKAKMTTAISIEDVREVKLLSLSGHKY 207

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0Y 232 GHNHNVKRYDACEGJLANYIMELCEGELLDRILARGARTEDDAAIYVOLLISVAF 291
Db 208 GHNHNPHTYDAIEHDHNVYIMELCEGELLDRILISGKRTEDDATWAIOLLNVAFC 267
0Y 292 HLOGVVRHDLKPENFLFTTRBDENAPMKLIDFGLSDFRDPERLNDIYGASVYVAPEVLR 351
Db 268 HLOGVVRHDLKPENFLFTSKSDTSQKLAIDEGLSDIYRDPERLNDIYGASVYVAPEVLR 327
0Y 352 SYSMEADWISGVITTYILLCSRPFWARTESGIFRSVLRADPNFEDSPMPVTSAAEKDFV 411
Db 328 SYSTEADWISGVIVYILLCSRPFWARTESGIFRAVLKADPSHDDPMPLLTSSERADFV 387
0Y 412 KRLNKDVRKRYMTAVOALTRHFWMLD-BQORIPDLIELFKILKOLYRATPKRLALAKLS 470
Db 388 KRLNKDPRKRLTYAOLASHPMILSDDAVPMPIITVEFKLMRAYLRSSLSRKALALAKLS 447
0Y 471 ALRDELLYTLKLOFKLEP-RDGVSLSDNFRATLTRYLDAMKESRYLEFLHLEPLAYR 529
Db 448 TLTVDELTYLEBQVALLPEPSKNGTISLENTKSKALMKKATAMKDSRIPELTGOLSALOYR 507
0Y 530 RMDPEECCAALISFYQLEBALERWEELIGTAPQOPEDEGNRVISVEELAOELNLAFT-HY 587
Db 508 RMDPEECCAALISYHOEALDRHQHARCAYELFEKEGNRPIMIDELASLGSPGVPH 567
0Y 588 SIYODWIRKSDKLNFTKPLHGVYIR 616
Db 568 AVLHMDLHRHDGKLSFLGFEVKKLHGAVSSR 596

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RESULT 6

calcium-dependent protein kinase homolog - carrot
C:Species: Daucus carota (carrot)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C:Accession: S60052
R:Lindzen, E.; Choi, J.H.
Plant Mol. Biol. 28, 785-797, 1995
A:Title: A carrot cDNA encoding an atypical protein kinase homologous to plant calcium-c
A:Reference number: S60052; MUID:95367641
A:Accession: S60052
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-602 <LIN>
A:Cross-references: EMBL:X83869; MID:g1103385; PDB:CAA58750.1; PID:e135087; PID:g1103388
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
C:Keywords: ATP
F:166-410/Domain: protein kinase homolog <LIN>
F:154-162/Region: protein kinase ATP-binding motif

[illegible][illegible]

RESULT 7

C:Calcium-dependent protein kinase-1like - Arabidopsis thaliana
 N:Alternate names: protein T8M16_90
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
 C:Accession: T51264
 R:Benes, V.; Wurmach, E.; Drzonek, H.; Ansoerg, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.
 submitted to the Protein Sequence Database, August 2000
 A:Reference number: 225346
 A:Accession: T51264
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-577 <BEN>
 A:Cross-references: EMBL:AL390921
 A:Experimental source: cultivar Columbia; BAC clone T8M16
 C:Genetics:
 A:Map position: 3
 A:Initons: 163/3; 206/2; 220/2; 256/3; 283/1; 382/1; 419/3; 455/3; 476/3; 532/3
 A:Note: T8M16_90
 A:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

| Query Match | Similarity | 56.1% | Score 1829 | DB 2 | Length 577 |
|-------------|------------|---|-------------------|----------------|------------|
| Best Local | Similarity | 56.7% | Pred. No. 7.8e-63 | | |
| Matches | 355 | Conservative | 100 | Mismatches 107 | Indels 64 |
| | | | | | Gaps 7 |
| QY | 1 | MCQCYGKGSAGSRTADDEGGVTEHOSPPRANGLPSRPQQAQAQOQGTPRRRGSKSG | 60 | | |
| Db | 1 | MCLHGK-----PIEQSKNLPISNIEETPKKSSOKAS----- | 35 | | |
| QY | 61 | STTPGHQTPGVAMPSPYPBSGASPLPA-----GVSPSPARSTPRRFKRPPEPSPAKH | 114 | | |
| Db | 36 | -----SGFPYSPSLPLSLFKTSPAAVSSSVSSSTPLRIFRRPRPPSPAKH | 81 | | |
| QY | 115 | IKATLAKRLGGCKPRKEGTTPEEGVGAGGGGGAADGAETERPDLDTKGFSKNFCAYEL | 174 | | |
| Db | 82 | IRALLARHHGSKYPMEASIP-----GSECEYGLDKKGFSGKOFASHYEI | 126 | | |
| QY | 175 | GKEVGRGHFGHCSAVVKKGEYKGTVAVKIIAKAKMTAISIEVYREVKILRLBSGHN | 234 | | |
| Db | 127 | DGEVGRGHFGYTCASAKKGGSLKGGDVAVKVIIPKSKMTTALIEVYRREVKILRLALTGHK | 186 | | |
| QY | 235 | NLVKRYDACEGLANVYIYMELOEGELLDLRIARGRTTEBPAAKAIYVOIISVAFCHQ | 294 | | |
| Db | 187 | NLVQYTDAPFEDDENAYIYMELOGGELLDLRIORGKTSVDAAKVMQIISVAVYCHQ | 246 | | |

[illegible]

RESULT 8

702105

calcium-dependent protein kinase (EC 2.7.1.1.) T3K9.9 - Arabidopsis thaliana

N:Alternate names: CPK-related protein; CPK-related protein kinase

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 26-Feb-1999 #sequence=revision 26-Feb-1999 #text_change 16-Feb-2001

C:Accession: T02105; C84838

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, February 1999

A:Description: Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence.

A:Reference number: Z14570

A:Accession: T02105

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-576 <R0U>

A:Cross-references: EMBL:AC004261; NID:g3402695; PIDN:AAD12016.1; PID:g3402722

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Snea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Mofeit, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.; Eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-769, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A04420; MUID:20083487

A:Accession: C84838

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-576 <STO>

A:Cross-references: GB:AE002093; NID:g3402722; PIDN:AAD12016.1; GSPDB:GMD0139

C:Genetics:

A:Gene: At2g41140; T3K9.9

A:Map position: 2

A:Intons: 161/3; 205/2; 219/2; 255/3; 282/1; 381/1; 418/3; 454/3; 475/3; 531/3

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C:Keywords: phosphotransferase; protein kinase

F:121-385/Domain: protein kinase homology <KIN>

| | | | | | | | | | |
|-----------------------|-------|--------------|---------|------------|--------|--------|----|------|---|
| Query Match | 55.7% | Score | 1816.5 | DB 2: | Length | 576 | | | |
| Best Local Similarity | 57.3% | Pred. No. | 2.3e-62 | | | | | | |
| Matches | 358 | Conservative | 95 | Mismatches | 109 | Indels | 63 | Gaps | 9 |

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QY 1 MGCCTGKAGSATTADDEGGVTTENMGSPRRANGLESTPRROQAQAQAQVGTFRKRSKSG 60
    |||
Db 1 MCGICGK-----PVEQDS-----KSLPISGETNAPLNQ----- 30
    |||

QY 61 STTPHQHTGVPAMPSPYDSCGASPLDAAVSPFA-----RSTPRFRFKRPPSPAKHI 115
    |||
Db 31 ----PRAKSSGGFPYSP-----SPVPSLFLKSSPSVSSVSTPRIRKRPKRPSPAKHI 81
    |||

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[illegible]

RESULT 9
 D96532
 probable CDPK-related protein kinase [imported] - *Arabidopsis thaliana*
 C.Species: *Arabidopsis thaliana* (mouse-ear cress)
 C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C.Accession: D96532
 R.Theologidis, A.; Ecker, J.R.; Palm, C.J.; Federpetel, N.A.; Kaul, S.; White, O.; Alonso,
 Chlin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000
 A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltl, R.; Merzla
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A.Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A.Reference number: AB6141; MUID:21016719
 A.Accession: D96532
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-606 <STD>
 A.Cross-references: GB:AE005173; NID:g10120419; PIDM:AMG13044.1; GSPDB:GN00141
 C.Genetics:
 A:Gene: F14U22.18
 A:Map position: 1

| | | | | |
|---------------------------|--------|--------------------|------------|-------------|
| Query Match | 54.08; | Score 1760.5; | DB 2; | Length 606; |
| Best Local Similarity | 59.78; | Pred. No. 3.2e-60; | | |
| Matches 357; Conservative | 74; | Mismatches 104; | Indels 63; | Gaps 11. |

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QY 64 PCHQTPGVAMPSPYPSCG-ASPLPAGVSDSPAR-----STPRRFK 103
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 32 PDH--PCKS-PIPTPSAAKASPPFPFYTTSPARHRRNKSADVGGGSEKSLSTPLQLR 88

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| | | | | |
|-----------------------|-------------------|--------------------|------------|-------------|
| Query Match | 35.48; | Score 1153.5; | DB 2; | Length 571; |
| Best Local Similarity | 40.88; | Pred. No. 2.6e-37; | | |
| Matches 257; | Conservative 103; | Mismatches 191; | Indels 79; | Gaps 11; |

Db 531 EADIDNDGKISLQFFRRLRLTASIKSRNVR 560

Db 531 EADIDNDGKISLQFFRRLRLTASIKSRNVR 560

Query Match 33.1%; Score 1080; DB 2; Length 516;

RESULT 11

T05500

calcium-dependent protein kinase homolog T19K4.200 - Arabidopsis thaliana

C.Species: Arabidopsis thaliana (mouse-ear cress)

C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000

C.Accession: T05500

R.Bevan, M.; Wedler, H.; Wambolt, R.; Hohelsel, J.; Mewes, H.W.; Mayer, K.F.X.; Schue

submitted to the Protein Sequence Database, April 1998

A.Reference number: Z15418

A.Accession: T05500

A.Molecule type: DNA

A.Residues: 1-536 <BEV>

A.Cross-references: EMBL:AL022373

A.Experimental source: cultivar Columbia; BAC clone T19K4

C.Genetics:

A.Map position: 4

A.Introns: 106/3; 150/2; 164/2; 198/3; 225/1; 281/3; 324/1; 362/3; 398/3; 419/3; 477/

A.Note: T19K4.200

C.Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein

C.Keywords: EF hand

F:69-328/Domain: protein kinase homology <KIN>

Best Local Similarity 42.6%: Pred. No.1,5e-34; Matches 232; Conservative 105; Mismatches 177; Indels 30; Gaps 8;

QY 88 GVSPPSPANSTRPRFFKRPFPSPPAKHILAKRLGGCKREKTEPBEGVGAGGGGG 147
Db 2 GLCFSSPKATRRGTSRRPNPDSPFTQKASEKVSNNKNNKKIQLRHGGGIPYG----- 56
QY 148 AADAEFRPLDRTFFGFSKNGAKYELCKEYGRGHFGHTCSAAYVKKGEYKQYAAVKIA 207
Db 57 -----KRID--FGAKKIDFDNRRTYIGKLLGHQGFET--YVATDNNNNRFAVKRID 103
QY 208 KAKMTAISIDVDRREVYILRALSGHNNLVKPYDACEGLNVVYIMELCEGGLDRLIA 267
Db 104 KAKMTPLLEVEDVREKVIILALGHEVYGFHNAFEDKTYIYIMELCDGGLDRLIA 163
QY 268 RGRYTEEDAKAIYVOLLISVAFCHLQGVHRDLKPNFLETTDENA PMKLIDFGISDF 327
Db 164 -NRYTEKDAAYVVRQMLKVAAECHLRGLVHRDMKPNFLEKSTEGSSLKATDFGLSDF 221
QY 328 IRPDRRLNDIYGSAYVAPEVLRHSYSMEADINSGVITYIILGSRFPARTSGTFRS 387
Db 222 IKPGVKFDIDYGSAYVAPEVLRHSYSMEADINSGVITYIILGSRFPARTSGTFRS 281
QY 388 VLRAADPNFDDSPMPVSAEAKDFVKRFNLKDYRKMTVVOALTPHMLD--EQROIPDI 445
Db 282 VMKRPDPREVPMPLISGAKADFYKKLLVKEPRARLTPAOLHSWSVKEGGEASEVPDI 341
QY 446 LIFRLIKOYLRATPLKRLALAKLSKALREDELLYKLOFKLE--PRDFVSLDNFRALT 504
Db 342 SVLNNMRQFVFSRLKQJALRALAKTINEDELDDLRQFDAMIDIDKNISISLEEKROLA 401
QY 505 RYLDAMKESRYLEPLALHLEPLATRRMDPEFCAAISPYOLEA--LERMEIAGTAFOQ 562
Db 402 KDVPKMLDARVAEILQANDSNTDOLVDTEFYVAALHVNOLDLEHDSKWOORSAKRAED 461
QY 563 FEOEGNRVYSVEU-----AOELNLAPTHYSIVODMIRKSGKINLFLEFTKFLGVTIRG 617
Db 462 PDIDDDGTTPEELRLNOCLOOTGLKSTIEPLLEADYDVEDGRISINEFRRLNSASLKS 521
QY 618 SNTR 621
Db 522 KNVK 525

RESULT 12
H84810
Probable calcium-dependent protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C:Accession: H84810
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: H84810
A:Molecule type: DNA
A:Residues: 1-583 <STC>
A:Cross-references: GB:AE002093; NID:93928078; PIDN:AACT9604.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g38910
A:Map position: 2
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C:Keywords: EF hand

Query Match 28.3%; Score 923.5; DB 2; Length 583;
Best Local Similarity 38.1%; Pred. No.1,3e-28;
Matches 217; Conservative 96; Mismatches 204; Indels 53; Gaps 16;

QY 53 RRRGSKS--GSTTPGHQTPGVAMPSPYRSGASPLPAGVSPSPANSTRPRFFKRPFPSPS 110

Db 42 RKKNDKSYNGDDSNCHVSYTV---DPAPS-----TLPTPTSPPPVVKMANDEEPPPK 89

QY 111 PAKHIKATLARIKLGGRK-P-KEGTIPBEGVAGAGGGGAADGAETERRPLDKTREG-FSKN 167

Db 90 P-----ITENKEDPNRSKPOKKKAHKRMAASAGL-----QIDSVLGKRTEN 129

QY 168 FGAKYTELCKEVRGRGHFGHTCSAVYAKGEGYKQOTYAVKIIAAKAKMTAISIEDVREVVIL 227

Db 130 LKDIYSVGRKKLGQGGFGFTPLCLVDK---TGKEFKAKTIAKRLTTPPDVEDVREIEM 186

QY 228 RALSGHNMLVCFYDACEDGLNANYIYMELCGEGELDLRIILARGRYTEDAKAIYQILSY 287

Db 187 HHLSSHPRVIOYGVACEDAVAVHYVMEICAGSELFDRIQR-GHTTEKKADELARIITGV 245

QY 288 VAFCHLGVVHRDLKPENFLFTTRDENAPMKLIDFGLSDFTRPDERLNDIVGSAYVAPE 347

Db 246 IEACHSLGVHRDLKPENFLFVSGDEBAALKTIDGLSVFEPKGETFTDVVGSPYVAPE 305

QY 348 VLHRSYSMEADIMISGVITTYTILCGSRFPFMAETEGITRSVLRADPNDDSPWPIVSAEA 407

Db 306 VLRRKHYSHCCVWSAGVIITYYILSGPFPFMEETEGIEQVYLGKGLDFISEPWPVSESA 365

QY 408 KDEVVRFLNKDQVRKRMATVVALTHPMLRDEQRQI--PDILILFRLIKOYLRTPLKRAL 465

Db 366 KDLVRMLIRDPKKRMTTHVEVLCHPMARVGYALDKPLDSAVLSLKLOQFSAMNKLKKTAT 425

QY 466 KALSKALREDELLYKLOFKLE--PRDGFVSLDNFRALTTRYLDAMESRYLEFLHALE 524

Db 426 KYIASLSSEELIAGLKEKFMKMTDONSCHITTEELKKGIDRVGAD-LKDSILGLMQAAD 484

QY 525 PLATRRMDPEEFCAAIISPYOLEALERNBELAGTAPFOOPEDGKNVYSVEELAQ---ELN 581

Db 485 IDNSGTIDYGERIAMV---HLNKIEK-EDHLFTAFSYFDQDGSQYITRDELQACQKQFG 540

QY 582 LAPTHY-SIYDWMIRKSDGKLNFLGFTKFL 610

Db 541 LADVHLDDLKREVNDKNDGRIDYSEFVDM 570

RESULT 13

S56652

C:calcium-dependent protein kinase (EC 2.7.1.-) 2 - rice

C:Species: *Oryza sativa* (rice)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-Jun-1999

C:Accession: S56652

R:Brevario, D.; Morello, L.; Giant, S.

Plant Mol. Biol. 27, 953-967, 1995

A:Title: Molecular cloning of two novel rice cDNA sequences encoding putative calcium

A:Reference number: S56651; MUID:95284352

A:Accession: S56652

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-533 <BRE>

A:CROSS-references: EMBL:X81394; NID:9587497; PIDN:CA57157.1; PID:9587498

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specif

F:83-343/Domain: protein kinase homology <KIN>

F:91-99/Region: protein kinase ATP-binding motif

F:385-417/Domain: calmodulin repeat homology <E1F>

F:421-453/Domain: calmodulin repeat homology <E2>

F:457-489/Domain: calmodulin repeat homology <E3>

F:492-524/Domain: calmodulin repeat homology <E4>

F:114/Active site: Lys #status predicted

Query Match 27.7%; Score 904.5; DB 1; Length 533;

Best Local Similarity 36.7%; Pred. No. 6.3e-28;

Matches 210; Conservative 91; Mismatches 194; Indels 77; Gaps 14;

QY 55 RSKSGG-----STPGHOPGVAMPSPYSGASPLPAGVSPAPRSRPRRRFKRPPPP 109

Db 15 RGAGNGYGHOTKPAQOTTPSYNHPP-----PPPAVYKTRTPSAMNP-----PVVP 61

```

QY 110 SPANKIKATLAKRLGGKPKKEGTIPREGGVAGGGGGAADGATERPDLKTFGSKNFG 169
|
Db 62 VVAP-----PKPTPTD-----GKLV---DVR 82
QY 170 AKELGKNGRGHGHNT--CSAVKKGKYGQTVAAKIIAKAMTAISIEDVREVKIL 227
|
Db 83 SVSLKEKELRGQGVYLTCTEIA-----SGKQACKSKSKRLVSKAKEDIRREIQIM 137
QY 228 RALSGNNLVKREYDACEEDGNNYIVMELCEGGLDRIIARGRTVEEDAKAIIVOILSV 287
|
Db 138 QHLSGQNNIVEFGATEDSNVHVMELCAGELFDRITAK--GHYSERAAATICRAVVAV 196
QY 288 VAECHLQGVNHRDLKPENFLETTREDENAPMKLIDELGSEFPDELDNIVASAVYVPE 347
|
Db 197 VNICHFMGVNHRDLKPENFLETTREDENAPMKLIDELGSEFPDELDNIVASAVYVPE 256
QY 348 VLRHSYSMADWISIGVITYILLCSGSPFWARTESGIFRSVLRADPNFDDSPMPTVSAEA 407
|
Db 257 VLKRNNGKIDVRSAGVILYITLISGVPWMAETKEGIFDALILOGELDESPQWPSISSA 316
QY 408 KDFVKRFLKDYRKRTAVQALTHPMLRD--EQROIPLDILFRILKQYLKATPLKRLAK 466
|
Db 317 KDLVRKMLQDPKRTTSQVQVQHPRMLNDGASDKPIDSAYLSRKQOFRAKKLKKALK 376
QY 467 ATSKALREBELLYLKLOFKLE--PRDGFVSLDNFRTALTRYLTDAKESRYLEFLHALEP 525
|
Db 377 VVASLNNEEIKGLKQMFNMDDNSGTITYEELKAGLAK--LGSRLSAEYKQMLEADY 435
QY 526 LAYRRADFEFCFAAISIPQLEALERMELIAGTAQOFEQGNRYISEL-----AOEL 580
|
Db 436 DENGSDIDVEFTTATMHRKLER---DEHLKAFQYFDKDNISGFTTRDELSALIEHEM 491
QY 581 NLAPHYSIVODMIRKSDGKLNFLGTFKPLNG 612
|
Db 492 GDTSTIKDIISEVDTDNDGRINYEFCAMRG 523

```

RESULT 14

calcium-dependent protein kinase (EC 2.7.1.-) 6 - Arabidopsis thaliana
 N:Alternate names: protein F9D16.120
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 14-May-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
 C:Accession: T05597; S71774; S71901; S71197
 R:Byron, M.; Medler, H.; Weiler, E.; Wandt, R.; Hohnsels, J.; Mewes, H.W.; Mayer, K.F.
 submitted to the Protein Sequence Database, February 1999
 A:Reference number: Z15419
 A:Accession: T05597
 A:Molecule type: DNA
 A:Residues: 1-529 <BEV>
 A:Cross-references: EMBL:AL035394
 A:Experimental source: Cultivar Columbia; BAC clone F9D16
 R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Chua, N.H.
 Plant Mol. Biol. 30, 1259-1275, 1996
 A:Title: Expression of three members of the calcium-dependent protein kinase gene family
 A:Reference number: S71774; MUID:96311013
 A:Accession: S71774
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1448, 'K', 450-529 <HON>
 A:Cross-references: EMBL:U20625
 R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.
 submitted to the EMBL Data Library, February 1995
 A:Description: Expression of the calcium-dependent protein kinase gene family in Arabid
 A:Reference number: S71197
 A:Accession: S71901
 A:Molecule type: DNA
 A:Residues: 1-529 <HON>
 A:Cross-references: EMBL:U20625; NID:9836943; PIDN:AAA67656.1; PID:9836944
 A:Accession: S71197
 A:Molecule type: mRNA
 A:Residues: 1-529 <HON>

A:Cross-references: EMBL:U20623; NID:9836939; PIDN:AAA67654.1; PID:9836940
 C:Genetics:
 A:Gene: CDPK6
 A:Map position: 4
 A:Introns: 137/2; 233/1; 281/1; 332/1; 370/3; 426/3; 469/2; 502/3
 A:Note: F9D16.120
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein
 F:76-336/Domain: protein kinase homology <KIN>
 F:84-92/Region: protein kinase ATP-binding motif
 F:379-411/Domain: calmodulin repeat homology <EF1>
 F:415-447/Domain: calmodulin repeat homology <EF2>
 F:451-483/Domain: calmodulin repeat homology <EF3>
 F:485-518/Domain: calmodulin repeat homology <EF4>
 F:107/Active site: lys #status predicted

Query Match 27.7% Score 903.5; DB 1; Length 529;
 Best Local Similarity 39.5% Pred. No. 6,9e-28;
 Matches 209; Conservative 91; Mismatches 178; Indels 51; Gaps 14;

```

QY 107 PPSPAK-----HIKATLAKRLGGKPKKEGTIPREGGVAGGGGGA-----DGAE 153
|
Db 13 PPSSSSSSGNNVNHVKNRAGER--GSSGSGT---GSSGSGTGSNSTTQONGRI 66
QY 154 TERLDTFGSKNFGKAYELGKVEGRGHGHTCSAVKKGKYGQTVAAKIIAKAMTT 213
|
Db 67 LGRMEEV-----RRTYFEGRELGRQGVYLVYTHKETK---QGVACKSIPTRLV 116
QY 214 AISEDVREVKILRALSGNNLVKRFYDACEEDGNNYIVMELCEGGLDRIIARGRT 273
|
Db 117 KDIEDVRRVQVIMHLSGSRNVYDLKAGEDVSHVNLMECEGGLDRIITK--GLYS 175
QY 274 EDAKAIIVOILSVAFCHLQGVNHRDLKPENFLETTREDENAPMKLIDELGSEFPDEPDR 333
|
Db 176 ERAAADLCROMVNVVHSCSMGVNHRDLKPENFLSKDENSPLKTDGELSVFFRPGDK 235
QY 334 LNDVGSAYVAVPEVLRHSYSMADWISIGVITYILLCSGSPFWARTESGIFRSVLRADP 393
|
Db 236 FKLVGSATYVAVPEVLRKNGPRAVDASGVILYITLISGVPWMAETKEGIFDALILOGEL 295
QY 394 NFDDSPMPTVSAEAKDFVRFKNDYRKRTAVQALTHPMLRD--EQROIPLDILFRIL 451
|
Db 296 DFGADPWPALSDGAKDLVRLKLYDKORLTAAEVNHPWREDEBASDKPLDNVLSRM 355
QY 452 KQYLRTPYKRLAKLAKSALREDELLYLKLOFKLE--PRDGFVSLDNFRTALTRYLTDA 510
|
Db 356 KQFRANKLKKKALKVIATNLESEELIGLEKEMFKSLTDNNIGVITLLELRTGLPK--LGSK 414
QY 511 MKESRYLEFLHALEPLAYRRMDFEFCFAAISIPQLEALERMELIAGTAQOFEQGNRY 570
|
Db 415 ISEAEIRQLEAADDGDSIDYLEFISITM---HNNRIER-EDILYLAFTAFDNDNSGY 470
QY 571 ISVEELAGLNLAPHYSIVODMIRKS-----DGKLNFLGTFKPL 610
|
Db 471 ITME---ELELAMKKNWGDGDSIKETIAYEVDTRDGRKINYEFEVAM 515

```

RESULT 15

calcium-dependent protein kinase (EC 2.7.1.-) CDPK - pumpkin
 N:Alternate names: calcium-dependent calmodulin-independent protein kinase CDPK
 C:Species: Cucurbita pepo (pumpkin)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T09940
 R:Ellard-Jones, M.; Hopkins, R.B.; White, T.J.; Lomax, T.L.
 Plant Mol. Biol. 39, 199-208, 1999
 A:Title: Cloning, expression and N-terminal myristoylation of CcpK1, a calcium-depen
 A:Reference number: Z16988; MUID:9918773
 A:Accession: T09940
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-573 <ELL>

A:Cross-references: EMBL:U90262; NID:g1899174; PIDN:AAB49984.1; PID:g1899175

A:Experimental source: etiolated hypocotyls

C:Genetics:

A:Gene: CPK1

C:Function:

A:Description: serine/threonine-specific protein kinase activated by direct binding of C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphotrans F:108-368/Domain: protein kinase homology <KIN>
F:447-479/Domain: calmodulin repeat homology <EFH>

```
Query Match          27.5%; Score 895.5; DB 2; Length 573;
Best Local Similarity 36.6%; Pred. No. 1.5e-27;
Matches 207; Conservative 98; Mismatches 205; Indels 55; Gaps 13;

QY 57 SKSGSTTPGHQTGVAMPSPYPSGASPLPAGYSPSPARSTPRFRFRPPSPAKHIK 116
   11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 SKTPENSVSHTGENREYVASEPSPLPVQNP--PEKYTMPESVAKPPPEPKYR-- 82
   26 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 117 ATLAKRLGGCKPKEGTPREGGVAGGGGAGADGAEETERPLDKTFGFSKNFGAKYELGK 176
   83 -----PVAKRVSAGLRGGSVLTQKT-----GNFKETYSLGK 114
   83 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 177 EVGRGHGHTCSAVKKGEYKQTVAVKIIAKAMTTAISIEDVRRREVKILRALSGHNL 236
   115 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 KLAGOGGTTCYMCVEKA---TGKEYACKSIARKRLVNEDEVREIQIMHLSGHPNV 171
   115 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 237 VKFYDACCEDLNNYIWMELDEGGEILDRIILARGRYTEEDAKAIVOILSVAFCHLGQV 296
   172 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 ISTKGAEEDVAOVVVELLACGGLFDRITQR-GHYTERKAELTRITVGLVLEACHALGV 230
   172 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 297 VHRDLKRENFLFTTRDENAMPKLIDFGLSDFIRPDERLNDIVGSAYVAPVLEHRSYSME 356
   231 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 231 MHRDLKRENFLFSKEESLTKTIDFGLSMFKRGEKFNVDYGSPIYVAPVLEHRSYSME 290
   231 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 357 ADIWSIGVTIYILCGSRPFWARTESGIFRSVLRADPNFDDSPWPTVSAEAKDFVKRFLN 416
   291 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 ADVWSAGVIYIILSGVPPFWASEEGIFEEVILHGDLDFFSDPWPISDSKDLVRRMLV 350
   291 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 417 KDYRKRTAVOALTHPMLRDE--QROIPLDILIPRLIKOYLRAATPLKRLALKALSKALRE 474
   351 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 351 RDRPKRLTAEVLCHPWVQYDVAAPDKLDSAVLTRLKQFSAMNKLKMAIKVIAESLSE 410
   351 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 475 DELLYLKIQFKLLE-PRDGEVSLDNFRTAATRYLTDMAKESRVLEFLHALEPLAYRRMD 533
   411 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 411 EETAGLKEMFKMIDTDSGQITFEELKAGLKKFGAN-LKSEIYDLMOADIDONGTIDY 469
   411 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 534 EEFCAAAISPYOLEALERMEELAGTAFQEPQEGNRIYSVEELAQEELNLAPTHYST---- 589
   470 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 470 GEFYAATL--HINKIIEKEDHLT-AAFSYFDKDSGFTIHDELQO---ACKKEGIEDLQ 521
   470 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 590 VQDMIRK----SDGKLNFLGFTKFL 610
   522 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 522 MEEMREVDQNDGSDIDYNEFVAMM 546
   522 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: May 2, 2002, 08:37:27
Job time: 7931 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2002, 08:40:21 ; Search time 71.84 Seconds
(without alignments)
317.959 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260

Sequence: 1 MGCCYKGCASRTADDEGV.....LGFTKFLHGVIRGSTRRH 623

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | ID | Description |
|------------|-------|---------|--------------|--------------|---------------------|
| 1 | 1894 | 58.1 | 602 | 1 CRK_DAUCA | P53661 daucus caro |
| 2 | 904.5 | 27.7 | 533 | 1 CDP2_ORYSA | P53663 oryza sativ |
| 3 | 877 | 26.9 | 610 | 1 CDP1_ARATH | Q06850 arabidopsis |
| 4 | 865 | 26.5 | 513 | 1 CDP2_MAIZE | P49101 zea mays (m |
| 5 | 847.5 | 26.0 | 532 | 1 CDPK_DAUCA | P28582 daucus caro |
| 6 | 817 | 25.1 | 508 | 1 CDPK_SORBN | P28583 glycine max |
| 7 | 794 | 24.4 | 542 | 1 CDP3_ORYSA | P53662 oryza sativ |
| 8 | 747 | 22.9 | 534 | 1 CDP1_ORYSA | Q14012 homo sapien |
| 9 | 505.5 | 15.5 | 370 | 1 KCC1_HUMAN | Q63450 rattus norv |
| 10 | 505.5 | 15.4 | 374 | 1 KCC1_RAT | P08414 mus musculu |
| 11 | 501 | 15.4 | 469 | 1 KCC4_MOUSE | P25323 dictyostell |
| 12 | 498 | 15.3 | 295 | 1 KMC4_DICDI | P13234 rattus norv |
| 13 | 495 | 15.2 | 474 | 1 KCC4_RAT | P27466 saccharomyc |
| 14 | 493.5 | 15.1 | 446 | 1 KCC1_YEAST | Q16566 homo sapien |
| 15 | 490 | 15.0 | 473 | 1 KCC4_HUMAN | P15751 rattus norv |
| 16 | 486 | 14.9 | 533 | 1 KCCD_RAT | Q13557 homo sapien |
| 17 | 484 | 14.8 | 499 | 1 KCCD_HUMAN | P53355 homo sapien |
| 18 | 470 | 14.4 | 1431 | 1 DAPK_HUMAN | P11275 rattus norv |
| 19 | 467.5 | 14.3 | 478 | 1 KCC4_RAT | P11798 mus musculu |
| 20 | 464.5 | 14.2 | 478 | 1 KCC4_MOUSE | Q38997 arabidopsis |
| 21 | 463.5 | 14.2 | 512 | 1 K110_ARATH | P07313 oryctolagus |
| 22 | 461 | 14.1 | 607 | 1 KMC1_RABIT | P015075 homo sapien |
| 23 | 461 | 14.1 | 740 | 1 DCK1_HUMAN | Q00771 emeticicella |
| 24 | 460.5 | 14.1 | 414 | 1 KCC1_EMENT | P28652 mus musculu |
| 25 | 458 | 14.0 | 542 | 1 KCCB_MOUSE | P20689 rattus norv |
| 26 | 455.5 | 14.0 | 609 | 1 KMCB_RAT | P08413 rattus norv |
| 27 | 455 | 13.9 | 542 | 1 KCCB_YEAST | P22517 saccharomyc |
| 28 | 454 | 13.9 | 447 | 1 KCC2_YEAST | Q09712 schistosach |
| 29 | 451.5 | 13.8 | 335 | 1 KCC1_SCHPO | P15753 homo sapien |
| 30 | 448 | 13.7 | 406 | 1 KPBH_HUMAN | O08875 rattus norv |
| 31 | 448 | 13.7 | 433 | 1 DCK1_RAT | Q13554 homo sapien |
| 32 | 447 | 13.7 | 664 | 1 KCCB_HUMAN | Q16816 homo sapien |
| 33 | 444.5 | 13.6 | 386 | 1 KPBG_HUMAN | |

| | | | | | |
|----|-------|------|------|--------------|--------------------|
| 34 | 443 | 13.6 | 382 | 1 KCC1_MEFAN | O14408 metarhizium |
| 35 | 440.5 | 13.5 | 406 | 1 KPBH_RAT | P31325 rattus norv |
| 36 | 438.5 | 13.5 | 386 | 1 KPBG_RABIT | P00518 oryctolagus |
| 37 | 438.5 | 13.5 | 397 | 1 S17A_RABIT | Q09m70 oryctolagus |
| 38 | 436.5 | 13.4 | 527 | 1 KCCG_RAT | P11730 rattus norv |
| 39 | 434.5 | 13.3 | 387 | 1 KPBG_RAT | P13286 rattus norv |
| 40 | 429 | 13.2 | 733 | 1 K6AA_XENLA | P10665 xenopus lae |
| 41 | 429 | 13.2 | 1906 | 1 KMS_CHICK | P11799 gallus gall |
| 42 | 427.5 | 13.1 | 415 | 1 KCCS_MALDO | O07250 malus domes |
| 43 | 427.5 | 13.1 | 1176 | 1 KMS_BOVIN | Q28824 bos taurus |
| 44 | 424.5 | 13.0 | 387 | 1 KPBG_MOUSE | P07934 mus musculu |
| 45 | 424.5 | 13.0 | 414 | 1 S17A_HUMAN | Q9uee5 homo sapien |

ALIGNMENTS

| RESULT | 1 | STANDARD | PRT | 602 AA. |
|-----------|--|----------|-----|--|
| CRK_DAUCA | | | | |
| ID | CRK_DAUCA | | | |
| AC | P53661 | | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | | |
| DT | 01-OCT-1996 (Rel. 34, Last sequence update) | | | |
| DT | 20-AUG-2001 (Rel. 40, Last annotation update) | | | |
| DE | CDPK-RELATED PROTEIN KINASE (EC 2.7.1.-) (PK421). | | | |
| GN | CRK. | | | |
| OS | Daucus carota (Carrot). | | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; | | | |
| OC | Asteridae; euasterids II; Apiales; Apiaceae; Daucus. | | | |
| OX | NCBI_Taxid=4039; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=CV. JUMAROT; | | | |
| RX | MEDLINE=95367641; PubMed=7640352; | | | |
| RA | Lindzen E., Choi J.H.; | | | |
| RT | "A carrot cDNA encoding an atypical protein kinase homologous to | | | |
| RT | plant calcium-dependent protein kinases." | | | |
| PL | Plant Mol. Biol. 28:785-797(1995). | | | |
| CC | - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. | | | |
| CC | CAMK SUBFAMILY. | | | |
| CC | - SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. ALL SEEMS | | | |
| CC | NON FUNCTIONAL. | | | |
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| CC | or send an email to license@sib-sib.ch). | | | |
| CC | ----- | | | |
| DR | EMBL: X83869; CA56750.1; - | | | |
| DR | HSSP: Q63450; 1A06. | | | |
| DR | InterPro: IPR002048; EF-hand. | | | |
| DR | InterPro: IPR000719; Euk_pkinase. | | | |
| DR | InterPro: IPR002290; Ser_thr_kin_actsite. | | | |
| DR | Pfam: PR00069; pkinase.1. | | | |
| DR | SMART: SM00220; S_TKC; 1. | | | |
| DR | PROSITE: PS00107; PROTEIN_KINASE_AMP; 1. | | | |
| DR | PROSITE: PS00108; PROTEIN_KINASE_ST; 1. | | | |
| DR | PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1. | | | |
| KW | Transferase; Serine/threonine-protein kinase; ATP-binding; | | | |
| KW | Repeat. | | | |
| FT | DOMAIN | 20 | 40 | 3 X 7 AA TANDEM REPEATS OF S-[LI]-P-X-X- |
| FT | REPEAT | 20 | 26 | D-X. |
| FT | REPEAT | 27 | 33 | 1. |
| FT | REPEAT | 34 | 40 | 2. |
| FT | DOMAIN | 148 | 410 | 3. PROTEIN KINASE. |
| FT | NP_BIND | 154 | 162 | ATP (BY SIMILARITY). |
| FT | BINDING | 180 | 180 | ATP (BY SIMILARITY). |
| FT | ACT_SITE | 276 | 276 | BY SIMILARITY. |

FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 1 (POTENTIAL)
 FT DOMAIN 502 513 ANCESTRAL CALCIUM SITE 2 (POTENTIAL)
 FT DOMAIN 542 553 ANCESTRAL CALCIUM SITE 3 (POTENTIAL)
 FT DOMAIN 574 585 ANCESTRAL CALCIUM SITE 4 (POTENTIAL)
 SQ SEQUENCE 602 AA: 67184 MM: 1D10BF68B3BF447 CRC64;

Query Match 58.1%; Score 1894; DB 1; Length 602;
 Best Local Similarity 60.4%; Pred. No. 1.9e-92;
 Matches 377; Conservative 89; Mismatches 122; Indels 36; Gaps 10;

QY 1 MGICVSK-----PSPEPDLHNHHTSIPIVND--TSLRP-QDNISIPKDLAIQAQDNK-- 49
 DB 1 MGICVSK-----PSPEPDLHNHHTSIPIVND--TSLRP-QDNISIPKDLAIQAQDNK-- 49
 QY 61 STTPGHQGTGVAMPSPYPS---GASPLPAGVSPSPASTRRFRFRFPSPSPAKHK 116
 DB 50 --PPGKSKSPFLPPYSPSPAHFLFSSKSPAVGSPAGSSNSTKRLE--PEPPSPSPAKHK 105
 QY 117 ATLAKLGGGKPKRECTIPEEGVGAGGGGAADGAETERPDKTFGFSKNGAKYELGK 176
 DB 106 AAMARRHGSVKKNEMALIPENNNEVDGAG-----LDKSGFSKNGKSGFEYGE 152
 QY 177 EYGRGHFGHTGSAVYKKGKQYQTAIVAKIATAKTATISIEDVREVKILRALSGHNL 236
 DB 153 EYGRGHFGHTGSAVYKKGKQYQTAIVAKIATAKTATISIEDVREVKILRALSGHNL 212
 QY 237 VKEFYDACEGLNVIYVMEICGEGELDRILANGRYTEEDAKAIYVOLLNVAAPCHLOGV 296
 DB 213 VOFYDAFEDHTNVVYVMEICGEGELDRILANGRYTEEDAKAIYVOLLNVAAPCHLOGV 272
 QY 297 VHRDLKPEFLETTDENAPMKLIDFGLSDFIRPDERLNDIVGSAVYVAPVLRHSYSME 356
 DB 273 VHRDLKPEFLETTDENAPMKLIDFGLSDFIRPDERLNDIVGSAVYVAPVLRHSYSME 332
 QY 357 ADIVSIGVITYLLCGSPENARTEGFRFVRADRPFDSPMPVSAEKDQVYKREFLN 416
 DB 333 ADVMSIGVITYLLCGSPENARTEGFRFVRADRPFDSPMPVSAEKDQVYKREFLN 392
 QY 417 KDYRRMTAVOALTHPMLRDEOR-QIPDLITIFRLIKOYLATPLKRLATKALSKALRED 475
 DB 393 KDYRRMTAVOALCHSWIKNSNDIKFPLDILVFLMKVYMSSPLRRAALRALSKITLTV 452
 QY 476 ELVYKLGQETLEP-ROGFVSLDNFRATLRYLTDANKESVLEFLHALBLEYLRMDFE 534
 DB 453 ELVYKLGQETLEP-ROGFVSLDNFRATLRYLTDANKESVLEFLHALBLEYLRMDFE 512
 QY 535 EFCAAAISPYOLEALERMEIAGTAFOQFEGNRSVSEVLELAQELMLAP--HYSIVOD 592
 DB 513 EFCAAAISVHQLALDRMEHARCAVYDLFEKDNRAIMIEELASGLGFSIPVHVALHD 572
 QY 593 WIRSDCKLNTLGTGTFKFLHGYTIR 616
 DB 573 WIRHTDGLSFLGYVKKLHGVSTR 596

RESULT 2
 CDP2.ORYSA
 ID CDP2.ORYSA STANDARD; PRT; 533 AA.
 AC P53683;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 2 (EC 2.7.1.-) (CDPK 2).
 GN CPK2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4536;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ARBORIO; TISSUE=Coleoptile;

RX MEDLINE-95284352; PubMed-7766885;
 RA Breviario D., Morello L., Gianti S.;
 RT "Molecular cloning of two novel rice cDNA sequences encoding putative
 RT calcium-dependent protein kinases."
 RL Plant Mol. Biol. 27:953-967(1995).
 CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
 CC INVOLVE CALCIUM AS A SECOND MESSENGER.
 CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
 CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAWK SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X81394; CAA57157.1; -
 CC HSSP; Q63450; 1A06.
 CC Interpro: IPR002048; Euk_Pkinase.
 CC Interpro: IPR000719; Ser_thr_kin.
 CC Interpro: IPR002290; Ser_thr_kin_actsite.
 CC Pfam: Pf00036; ehand; 4.
 CC Pfam: Pf00069; pkinase; 1.
 CC SMART; SM00220; S_TKc; 1.
 CC PROSITE: PS0018; EF_HAND; 4.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS50111; PROTEIN_KINASE_DOM; 1.
 CC KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC Calcium-binding; Phosphorylation; Multikinase family.
 CC FT DOMAIN 85 343
 CC NE_BIND 91 99
 CC BINDING 114 114
 CC ACT_SITE 209 209
 CC CA_BIND 398 409
 CC CA_BIND 434 445
 CC CA_BIND 470 481
 CC CA_BIND 505 516
 CC SEQUENCE 533 AA: 59522 MM: D0BC570ABD285E28 CRC64;

Query Match 27.7%; Score 904.5; DB 1; Length 533;
 Best Local Similarity 36.7%; Pred. No. 1e-40;
 Matches 210; Conservative 91; Mismatches 194; Indels 77; Gaps 14;

QY 55 RGSKSG-----STTPGHQGTGVAMPSPYPSGASPLPAGVSPSPASTRRFRFRFPSP 109
 DB 15 RGSAGYGTSHQTPAQOTTPSYNHPD-----PPPAEVRYTPSAMP-----PVVPP 61
 QY 110 SPARKIKATLAKRLGSGKPKRECTIPEEGVGAGGGGAADGAETERPDKTFGFSKNG 169
 DB 62 VVAP-----PKTPPTI-----LGKLY---DVR 82
 QY 170 AKYELGKYGKRGHFGHT--CSAVVKKGEYKGTQVAVKIAAKMTATISIEDVREVKIL 227
 DB 83 SVYSLGKELGRQGFVLYLCTEIA-----SGQYACKSISKRLKLVSKADKDIREIQIM 137
 QY 228 RALSGHNNLVKRYDACEGLNVIYVMEICGEGELDRILANGRYTEEDAKAIYVOLLISV 287
 DB 138 QHLSQOQNIIVERGAYEDKSNVHVMEICAGGELFDRIIAA-GHYSERAATITIRAVVNV 196
 QY 288 VAFCLOGVHRDLKPEFLETTDENAPMKLIDFGLSDFIRPDERLNDIVGSAVYVAPV 347
 DB 197 VNICHFMGVHRDLKPEFLETTDENAPMKLIDFGLSDFIRPDERLNDIVGSAVYVAPV 256
 QY 348 VLHRSMEADIVSIGVITYLLCGSPENARTEGFRFVRADRPFDSPMPVSAEA 407

```
Db 257 VLARNYKGEIDVMSAGVILYLLSGVPPPEWMAETKGFDAIILGGEIDFESQPMPSISESA 316
OY 408 KDEVKEPLNKDYKRMRTAVOALTHPMLRD-EQROIPDLILFRLIKOYLATPLKRLAK 466
Db 317 KDEVRAKMLTODPKRITTSOAVLOHPMLRDEASADKPLDSAVLSRMKOFKAMNKLKMAK 376
OY 467 ALSKALREDELTYLKLQFKLLE-PRDGFVSLDNFRRLATPRTYLDAMKESHYLEFLHALP 525
Db 377 VIASNLNEEIKGLKQMTFMDTDSNGTITYEELKAGLAK-LGSKLSEAVKQLEADY 435
OY 526 LAYRRMDFEECAAISPYOLEALERMEEIAGTAFOQFEGEGNRVISEEL-AGEL 580
Db 436 DNGSIDYVEFTATNHRHLER---DEHIFKAFOYFKDKNSGTFRDELSALIEHEM 491
OY 581 NLAPTHYSIVODMIRKSDGKLNFLGFTKFLHG 612
Db 492 GDTSTIKDITSEVDTDNDGRINTEFCAMRG 523

RESULT 3
CDP2_LARATH STANDARD: PRT; 610 AA.
AC 006850;
AD 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCULUM-DEPENDENT PROTEIN KINASE, ISOBFORM AK1 (EC 2.7.1.-) (CDPK).
GN AK1 OR AT5G04870 OR MUK11.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RC MEDLINE=93213795; PubMed=7916621;
RA Harper J.F., Binder B.M., Sussman M.R.;
RT "Calcium and lipid regulation of an Arabidopsis protein kinase
RT expressed in Escherichia coli."
RL Biochemistry 32:3282-3290(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RX MEDLINE=98162728; PubMed=9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned P1 clones."
RL DNA Res. 4:401-414(1997).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN MOUSE-EAR
CC CRESS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
CC EMBL: L14771; AAA32761.1; -.
CC DR EMBL: AB008271; BAB08991.1; -.
CC DR PTR: A49082; A49082.
CC DR HSSP: P02588; 1PON.
```

```
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00036; ehand; 4.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00054; EFh; 4.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00018; EF_HAND; 4.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Serine/threonine-protein kinase family.
KW Domain
FT DOMAIN 150 408 PROTEIN KINASE.
FT BINDING 156 164 ATP (BY SIMILARITY).
FT ACT_SITE 179 179 ATP (BY SIMILARITY).
FT CA_BIND 274 274 BY SIMILARITY.
FT CA_BIND 464 475 EF-HAND 1 (POTENTIAL).
FT CA_BIND 500 511 EF-HAND 2 (POTENTIAL).
FT CA_BIND 536 547 EF-HAND 3 (POTENTIAL).
FT CA_BIND 570 581 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 610 AA; 68253 MW; 41868DF12B0DF9FB CRC64;

Query Match 26.9%; Score 877; DB 1; Length 610;
Best local Similarity 37.5%; Pred. No. 3.2e-39;
Matches 196; Conservative 98; Mismatches 179; Indels 50; Gaps 12;

OY 104 RPPPP--PSPAKHIKATLAKRLGGRKEGTIPREGVGAGGGGGAADGAETERPDKT 161
Db 112 KPDPAPKPKPKHKRY-----SSAGLRRESVQRK 142
OY 162 FGFSKNGAKYELECKEGRGHGHTCSAVYKKGQYAVAKIIRAKMTAISIDVR 221
Db 143 ---TENKFEYSIGRKLGQGFITPLCEVT---TKERACKSIARAKLTIDVEDVR 196
OY 222 REVKILRALSGHNNLVKFYACEDGLNVYIVMELCEGELDRILRAGRYEDAKAY 281
Db 197 REIIMHHLAGHPVVISIKGAEVDYAVHLVMECCAGELFDRIQR-GHYTERKKAELT 255
OY 282 VOILSVAFCHLQGVNRDLKPENFLTTTRDENAPMKLIDFGLSDFRPDERLNDIYGA 341
Db 256 RTIGVVEACHSLGVHRDLKPENFLSVSKHEDLTLTIDFGSLMFKPDDVDFDVVGGSP 315
OY 342 YVVAPEVLHYSMEADVMSIGVTYILLGSRPFMAKRTSGIRSVLRADPNFDSPPM 401
Db 316 YVVAPEVLKRYGPEADVMSAGVITVLLSGVPPPEWMAETEGITEOVLHGDLDSPPMP 375
OY 402 TVSAEKDFVAKRFLNKDYRKRMRTAVOALTHPMLRD-EQROIPDLILFRLIKOYLATP 459
Db 376 SISESAKDVLKMLVRDPKRLTAHQVLCHPWQVDGVAAPDKPLDSAVLSRMKOFAMNK 435
OY 460 LKRLALALSALREDELTYLKLQFKLLE-PRDGFVSLDNFRRLATPRTYLDAMKESVLE 518
Db 436 FKKAALRVIAESIEEELAGIKEMFNIMIDAKSQITFEELKAKLRGAG-LKESELID 494
OY 519 FLHALPELAYRRMDFEECAAISPYOLEALERMEEIAGTAFOQFEGEGNRVISEELAQ 578
Db 495 LMQAADVDSNGTIDYKEFIATL---HLKTER-EDHLFAFTYFDKDGSGYITPDELQ 550
OY 579 ---ELNLAPTHY-SIVODMIRKSDGKLNFLGFTKFLHGVTIRG 617
Db 551 ACEFGEVDVIEELMRVDQDNDGRIDYNEFVAMQSGSITG 593

RESULT 4
CDP2_MAIZE STANDARD: PRT; 513 AA.
AC P49101;
AD 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCULUM-DEPENDENT PROTEIN KINASE 2 (EC 2.7.1.-) (CDPK 2).
```

GN CDPK2.
 OS zea mays (maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. MERRIT; TISSUE=Root tip;
 RX MEDLINE=95281563; PubMed=7761420;
 RA Patti S., Takekawa D., Poovaiah B.W.;
 RT "Chimeric plant calcium/calmodulin-dependent protein kinase gene with
 a neutral vishin-like calcium-binding domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:4897-4901(1995).
 CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
 INVOLVE CALCIUM AS A SECOND MESSENGER.
 CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
 CC AUTOPHOSPHORYLATION MAY PLAY AN IMPORTANT ROLE IN THE REGULATION
 OF THE KINASE ACTIVITY (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U28376; AAA69507.1; -
 DR HSSP: Q63450; 1A06.
 DR MaizeDB: 56895; -
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR000719; Euk. pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00036; ehand; 4.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00054; EFh; 4.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; EF_HAND; 4.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Calcium-binding; phosphorylation.
 FT DOMAIN 65 323
 FT NP_BIND 71 79
 FT BINDING 94 94
 FT ACT_SITE 189 189
 FT CA_BIND 379 390
 FT CA_BIND 415 426
 FT CA_BIND 451 462
 FT CA_BIND 486 497
 FT SEQUENCE 513 AA; 58081 MW; 235a61630CAC36 CRC64;

Query Match 26.5%; Score 865; DB 1; Length 513;
 Best Local Similarity 37.0%; Pred. No. 1, le-38;
 Matches 194; Conservative 92; Mismatches 198; Indels 40; Gaps 10;

QY 99 RREFKRPFPSPAKHITATLAKRLGGKPKKEGTPEEGVGAGGGGAGDAAEFERP 158
 DB 11 RRLKRLRYNPPQAAEVRTPSATNSAVPVAVPPK-----PTADTTL 54
 QY 159 DKRGSKNGANYELGKGVGHFGHT--CSAVVKKGEYKQGVAVKIITAKAKTTAIS 216
 DB 55 GKQY---EDVRYYSFGKEKLGRCGFVTLCTEIA-----SGQYVACKSKSKKLVSAD 106
 QY 217 IEDVREVKIPLALSGHNNLVKRYDCEDGLANYIYMELCGEGELLDRILANGRYTEED 276
 DB 107 REDIRREIOMHLSQPNVIFERFAGYEDKSNVHVVMELCAGELFDRIIAK-GHYTERA 165

QY 277 AKAIWOLISVVAFCFCHGVHROLDKPNFLETTTREDNAPKMLIDFGLSDFIRPERLND 336
 DB 166 AATICRAVYNNVYNICHFGVWNRDLKPNFLATNEENAMKADDFGLSVTEIECKMYRD 225
 QY 337 IVGSAVYVAPEVLNRSYSMEADIMSIGVITYILLGCSPPFARTEESGFJRVLRADPNFD 396
 DB 226 IYGSAYVAPEVLNRSYSMEADIMSIGVITYILLGCSPPFARTEESGFJRVLRADPNFD 285
 QY 397 DSPMFTVAEKDFYKRLNMDYKRRMAYVALHPWLRD--EORQPLDILFRILKQY 454
 DB 286 SOPMFTVISESADLVKRLTDPKRLTSADVLOHWRREGGEASDPRIDSAVLSRMKQF 345
 QY 455 LRATPLKRLALKALSKALREDELTYLKLQFKLE-PRGFVSILNFPALTRYLTDMKE 513
 DB 346 RAMNKLKMLKALVYASNLNEEIKGLKQMFNMOTDNGSTTYEELKAGLAK-LGSKLSE 404
 QY 514 SRVLEFLHALDEPLAYRRMDFEEFCAALISPYOLEALREMEIAGTAQOFEQEGNRYISV 573
 DB 405 AEVQOLMEADVDNGSIDYEFITATWHRKLER---DEHLFKARQYFDKNSGFTIR 460
 QY 574 EEL-----AOELNLAPTHYSIVODWIRKSGKLNFLGFTFLNG 612
 DB 461 DELESALIEHMGDTSTIREITSEVTDNDGRINVEEFCAMRG 504
 RESULT 5
 ID CDPK_DAUCA STANDARD; PRT; 532 AA.
 AC P28582;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALCIUM-DEPENDENT PROTEIN KINASE (EC 2.7.1.-) (CDPK).
 OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; easterids II; Apiales; Apiaceae; Daucus.
 NCBI_TaxID=4039;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choi J.H.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RX MEDLINE=92003674; PubMed=1912486;
 RA Suen K.-L., Choi J.H.;
 RT "Isolation and sequence analysis of a cDNA clone for a carrot
 calcium-dependent protein kinase: homology to
 calcium/calmodulin-dependent protein kinases and to calmodulin."
 RL Plant Mol. Biol. 17:581-590(1991).
 CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
 INVOLVE CALCIUM AS A SECOND MESSENGER.
 CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
 PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X56599; CA3936.1; -
 DR PIR: S17759; S17759.
 DR HSSP: Q63450; 1A06.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.

| SO | SEQUENCE | 532 AA: | 60065 MM: | F03BEF0360A0E348 CRIC4; |
|----|--|---------|-----------|-------------------------|
| DR | Pfam: PF00036; eHand: 1 | | | |
| DR | Pfam: PF00069; pkinase: 1 | | | |
| DR | SMART: SM00054; Eph: 4 | | | |
| DR | SMART: SM00220; S_TKc: 1 | | | |
| DR | PROSITE: PS00018; EF_HAND: 4 | | | |
| DR | PROSITE: PS00107; PROTEIN_KINASE_ATP: 1 | | | |
| DR | PROSITE: PS0108; PROTEIN_KINASE_STY: 1 | | | |
| DR | PROSITE: PS50011; PROTEIN_KINASE_DOM: 1 | | | |
| KW | Transtferase; Serine/threonine-protein kinase; ATP-binding | | | |
| FT | Calcium-binding; Phosphorylation. | | | |
| FT | DOMAIN | 81 | 339 | PROTEIN KINASE. |
| FT | NP_BIND | 87 | 93 | ATP (BY SIMILARITY). |
| FT | BLINDING | 110 | 110 | ATP (BY SIMILARITY). |
| FT | ACT_SITE | 205 | 205 | BY SIMILARITY. |
| FT | CA_BIND | 395 | 442 | EF-HAND 1 (POTENTIAL). |
| FT | CA_BIND | 431 | 406 | EF-HAND 2 (POTENTIAL). |
| FT | CA_BIND | 465 | 476 | EF-HAND 3 (POTENTIAL). |
| FT | CA_BIND | 500 | 511 | EF-HAND 4 (POTENTIAL). |
| SO | SEQUENCE | 532 AA: | 60065 MM: | F03BEF0360A0E348 CRIC4; |

| | | | | |
|---------------------------|--------|--------------------|------------|-------------|
| Query Match | 26.0%; | Score 847.5; | DB 1; | Length 532; |
| Best Local Similarity | 36.5%; | Pred. No. 9.6e-38; | | |
| Matches 201; Conservative | 95; | Mismatches 189; | Indels 65; | Gaps 14 |

[illegible]

| | | | |
|------------|-------------|-----------|-------------------------|
| RESULT | 6 | | |
| CDPK_SOYBN | | | |
| ID | STANDARD; | PRT; | 508 AA. |
| AC | P25683. | | |
| DT | 01-DEC-1992 | (rel. 24, | Created) |
| DT | 01-DEC-1992 | (rel. 24, | Last sequence update) |
| DT | 20-AUG-2001 | (rel. 40, | Last annotation update) |

```

Db 141 TIVEVEACHSLGVNHRDLKPFENLEFDIDEDAKLAKTDGLSLFYFPGSEFCDVGSPT 200
Oy 343 YVAPEVLHRSYSMEADISIVITYITLLCGSRPFWANTESGERSVLADPNFDDSPMT 402
Db 201 YVAPEVLHRSYSMEADISIVITYITLLCGSRPFWANTESGERSVLADPNFDDSPMT 402
Oy 403 VSAAKDFVKKRFLNKDYKRRMTAVQALTHPMLRDEQ--RQIPDILIFRLIKYLRATPL 460
Db 261 ISDSAKDLIRKMLDQNKRTLRITAEVLRHWIYDDNAPKPLDSAVLSRLKQFSAMNKL 320
Oy 461 KRLAKLSKRLKREDELLYLKLOFLE--PRDGFVSLDNFRALTRYLTDAMKESVLEF 519
Db 321 KKMALRYAERLSEELGKLEFKMIDTNSGTFTEDELKDKLKRVSLEL--ESEIKDL 379
Oy 520 LHALEPLAYRRMDFEEFCAAIISPYOLEALRMEELIAGTFOFEDGKRVISVEELAO- 578
Db 380 MDADADIKSGTIDYGEIATV---HLNKLREELNV-SAFSYFDKDGSGYITLDEIQQA 435
Oy 579 --ELNLAPTHYSIVQDMIRK---SDGKLNFLGFTKFL 610
Db 436 CKDFGLDDIH---IDMKIRIIDDNDGQIDYGEFAMM 470

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RESULT 7

CDP3_ORYSA STANDARD: PRT; 542 AA.

```

AC P53684;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCULUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (EC 2.7.1.-) (CDPK 11).
GN CPK11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ARBORIO; TISSUE=coleoptile;
RA MEDLINE=95284352; PubMed=7766885;
RT Breviarlo D., Morello L., Giant S.;
RT "Molecular cloning of two novel rice cDNA sequences encoding putative
RT calcium-dependent protein kinases.";
RL Plant Mol. Biol. 27:953-967(1995).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CANK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. THREE OF
CC THEM SEEM TO BE NON FUNCTIONAL.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR HSP: X81393; CAA57156.1; -
DR HSP: O63450; JAO6.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00036; ehand; 4.
DR Pfam: PF00069; kkinase; 1.
DR SMART: SM00054; Erb; 3.
DR SMART: SM00220; S_NG; 1.
DR PROSITE: PS00018; EF_HAND; 1.

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DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multisubunit family.
FT DOMAIN 79 337 PROTEIN KINASE.
FT NP_BIND 81 89 ATP (BY SIMILARITY).
FT BINDING 107 107 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 393 404 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 429 440 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT CA_BIND 499 510 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 542 AA; 6116 MW; D4D257275C126DDA CRC64;

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Query Match 24.4%; Score 794; DB 1; Length 542;
Best Local Similarity 34.6%; Pred. No. 6.2e-35;

Matches 185; Conservative 101; Mismatches 189; Indels 60; Gaps 13;

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Oy 125 GAKREGIT-----PEEGVGAGGGGGGAGADGAETFRPLDKTFGSKNF----- 168
Db 2 GNOCNGTIGSDYHNRPREHAGVYOG-----DSYLDLKKFDTPWEVNNFKPTASTIL 56
Oy 169 -----GAK-----YELGKEVGRHGHGT--CSAYVKKGEYVGGTVAAKIIA 207
Db 57 RRGIDPTISYVLRKKTADLRHRYITIGRKLQAOFGTYLCTEINTGCEY-----ACKTIP 111
Oy 208 KAKMTAISIEDVREVKILRALSGHNNLVKFDACEDGLNVIYVMELEGSELRLRIIA 267
Db 112 KRLITREDEVDVAREIQIHNLHSGHKNVVAINDYEDGGAIVHVELCAGGLFPRIOE 171
Oy 268 RGGVTEDEDAKAIYVOLLVYAFCHLQGVVHRDLKPNLEFTRDENAPKLLIDFGLSDF 327
Db 172 K-GHYSERRKAELRIIVSIVAMCHSLGVNHRDLKPFENLEFDIDEDAKLAKTDGLSLFY 230
Oy 328 IRPDERLNDIVGSAYYVAPVLRHSYSMEADISIVITYITLLCGSRPFWANTESGERS 387
Db 231 FKPGQVTELVGSPYYVAPVLRKRGPESDVSAGVILYLSGVPPWAETQOQIFDA 290
Oy 388 VLRADPNFDDSPMTVSAEKDFVKKRFLNKDYKRRMTAVQALTHPMLRDE--ORQIPLDI 445
Db 291 VLGKHIIDFQSDPMPKISDSAKDLIRKMLSHCPSERLKAHEVLRHPICNGVATQADLP 350
Oy 446 LIFRLIKOYLRATPLRKLALSKALREDELLYLKLOFLEPRD--GVFSLDNFRALT 504
Db 351 SVLSRLKQFSAMNKLKRLALRYAERLSEELAGLEMEKAVDTKRGVITFGELREGIR 410
Oy 505 RYLTDMKESRYLEFLHALEPLAYRRMDFEEFCAAIISPYOLEALRMEELIAGTFOFEE 564
Db 411 RFGEAE-FKDPTEIDIMEAHNNNNVTIHYEFRIATL---PLNKIEREHL-ANFTYFD 465
Oy 565 QEGNRYISVELEAOLNLAPTHYSIVQDWI---RKSDGKLNFLGFTKFLHGVTTI 615
Db 466 KDSGGYITVDKLORACGEHNMEDSLLEIISVDDNDQIDYAEFVAMQGSNV 520

```

RESULT 8

CDP1_ORYSA STANDARD: PRT; 534 AA.

```

AC P53682;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCULUM-DEPENDENT PROTEIN KINASE, ISOFORM 1 (EC 2.7.1.-) (CDPK 1).
GN SPK.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;

```


| Query Match | Best Local Similarity | Matches 176, Conservative | Score 747, DB 1, Length 534, Pred. No. 1,8e-32, Mismatches 184, Indels 30, Gaps 13, |
|-------------|--|---------------------------|---|
| 146 | GGAAGCAETGERLDTKTCFG-SKNFCAKXELKEGVEGRGHGH--CSAVYKKGEGYGGQYVA | 202 | |
| 49 | GALRGGLNLKSFV---LGIKTPNVRBELTLTGRELIDQGGQKTYLDTETSTGCQY-----A | 100 | |
| 203 | VKIIAKAKMTTAISIEDVAREVKILRALSGHNHLVKFEDACEDGILNVIYVMELCGEGELL | 262 | |
| 101 | CKTILKSNLRCSDEIEDVAREIQTJHNLISGCKNNIYITINDTYEDQAHVHVMELKAGGELL | 160 | |
| 263 | DRILARGCHYTEEDAKAIVVQILSVAFCHLOGVVHRDLKPNENLFTTRDENAPKKLIDF | 322 | |
| 161 | SKIQKR-GHYSERKAAELIKITVIGIECHSHGVNHRDLKPNENLFLDADDEFYSKVIDF | 219 | |
| 323 | GLSDTFRPDERLNDIVGSAVYVAPVLRHSYEMADINSIGVTIYLIGSGRPFWARTS | 382 | |
| 220 | GLSTVFRRQGVREYVSGSYTYIAPEVLEKRYGPEADIMTAGIYLVLLTGVPFWADIOS | 279 | |
| 383 | GIFRSVLRADPNFDDSPWVTYVSAEAKDFVKRLNDRKRMVAVALTHPLWRDE--ORQ | 440 | |
| 280 | GYEYVYLDGRIDRFCKNNRMPRISDSAKDLIKMLCYPLERIKLAHVLEKPKRMDGNGVATN | 339 | |

| ID | NAME | STANDARD | PRT | 370 AA. |
|----|--|----------|-----|---------|
| DT | 15-JUL-1998 (Rel. 36, Created) | | | |
| DT | 15-JUL-1998 (Rel. 36, Last sequence update) | | | |
| DT | 20-AUG-2001 (Rel. 40, Last annotation update) | | | |
| DE | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) | | | |
| DE | (CAM KINASE I). | | | |
| GN | CAMK1. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_Taxid=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=95369239; Pubmed=7641687; | | | |
| RA | Haribabu B., Hook S.S., Selbert M.A., Goldstein E.G., Tomhave E.D., | | | |
| RA | Edelman A.M., Snyderman R., Means A.R.; | | | |
| RT | "Human calcium-calmodulin dependent protein kinase I: cDNA cloning, | | | |
| RT | domain structure and activation by phosphorylation at threonine-177 | | | |
| RT | by calcium-calmodulin dependent protein kinase I kinase."; | | | |
| RL | EMBL J_14:3679-3686(1995) | | | |
| CC | - FUNCTION: PHOSPHORYLATES SYNAPSTIN I. | | | |
| CC | - CATALYTIC ACTIVITY: ATP + A PROTEIN - ADP + A PHOSPHOPROTEIN. | | | |
| CC | - ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE | | | |
| CC | PHOSPHORYLATED TO BE MAXIMALLY ACTIVE. | | | |
| CC | - SUBUNIT: MONOMER. | | | |
| CC | - TISSUE SPECIFICITY: UBIQUITOUS. | | | |
| CC | - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. | | | |
| CC | CAMK SUBFAMILY. | | | |
| CC | ----- | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration | | | |
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| CC | or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| DR | EMBL, L41816; AAA99458.1; - | | | |
| DR | HSSP: 063450; 1A06. | | | |
| DR | MIM: 604998; - | | | |
| DR | InterPro: IPR000719; Euk_pkinase. | | | |
| DR | InterPro: IPR002290; Ser_thr_kin_actsite. | | | |
| DR | Pfam: PF00069; pkinase; 1. | | | |
| DR | SMART; SM00220; S_TTC; 1. | | | |
| DR | PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. | | | |
| DR | PROSITE; PS00108; PROTEIN_KINASE_ST; 1. | | | |
| DR | PROSITE; PS00011; PROTEIN_KINASE_DOM; 1. | | | |
| KW | Transferase; Serine/threonine-protein kinase; Calmodulin-binding; | | | |
| KW | phosphorylation; ATP-binding; Alternative splicing. | | | |
| FT | Domain 20 276 PROTEIN KINASE. | | | |
| FT | Domain 287 321 CALMODULIN-BINDING (BY SIMILARITY). | | | |
| FT | NP_BIND 26 34 ATP (BY SIMILARITY). | | | |

[illegible]

```

FF CONFLICT      302      302      N > T (IN REF. 2).
SQ SEQUENCE     469 AA;  52627 MM;  CEIP98670822F975 CRC64;

Query Match          15.4%; Score 501; DB 1; Length 469;
Best Local Similarity 35.9%; Pred. No. 1.le-19;
Matches 120; Conservative 57; Mismatches 109; Indels 48; Gaps

QY 105 PPPPPSPAKHIKATLAKRLGGGKRKEGTPEEGGVGAGCGGAGADCAETEPRLDKTFGE 164
    | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   7 PCCSSPSCSYTAS-----TENLVDPYW-----IDGSND-PL----- 38
QY 165 SKNGCAKLELKVEGRGHFGHTCSAAVVKKGYSK--OTVAVKIIIAKKMTAISIEDVR 222
    | : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   39 ----GDFEVESESLRG----AJSIYRCKQKQTPALVKVLK-----TYDKKIVRT 84
QY 223 EVKIILRALSGHNNNVKFFDACEDGLANVIYIMVELCEGELDRILARGCRTEDAKAIVV 282
    | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   85 EIGVTLRLS-HPIIKKLKEIFETPELSIVELVTGSELDRIVEK-GYSEDADAIVK 142
QY 283 QILSVAFCHLGAVVHRDLKENFLFTTRDENAPMKLIDFGLSDFIPTDERLDIVGSAY 342
    ||| ||| : | : | | | | | | | | | | | | | | | | | | | | | | | |
Db   143 QILEVAALAHENGSIYHRDLKPENLLVYTPAPDAFLKIDAGLSKIVHQVMKTVCSTPG 202
QY 343 YVAPRVNLR-SYSMEADIWISGVTITILLGSRPFM-AFRESGFERSVLADNPDSPW 400
    | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   203 YCAPFILGCGATGPVEDMVSGIITVYLICGFEFPYERGDQFMFRILNCETYFISPWW 262
    ||||| ||| : | : | | | | | | | | | | | | | | | | | | | | | | |
QY 401 PTVASAEAKDPFKRKFLNKDYRRKMTAVOALTHPWL 434
Db   263 DEVSLNAKDLYKKLIYLDPKRKLTTFQALQHPMV 296
    || ||| ||| : | : | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
KMJC-DICDI STANDARD; PRT; 295 AA.
AC P25323:
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).
GN MKKA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=91340753; PubMed=1651931;
RA Tan J.L., Spudich J.A.;
RT "Characterization and bacterial expression of the Dictyostelium
RT myosin light chain kinase cDNA. Identification of an autoinhibitory
RT domain."
RL J. Biol. Chem. 266:16044-16049(1991).
RN [2]
RP REVISIONS.
RA Spudich J.A.;
RL Submitted (AUG-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE.
RC STRAIN=AX3;
RX MEDLINE=90337997; PubMed=2380188;
RA Tan J.L., Spudich J.A.;
RT "Dictyostelium myosin light chain kinase. Purification and
RT characterization."
RL J. Biol. Chem. 265:13818-13824(1990).
CC -I- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
CC MYOSIN LIGHT CHAIN.
CC -I- CATALYTIC ACTIVITY: ATP + [MYOSIN LIGHT-CHAIN] = ADP + [MYOSIN
CC LIGHT-CHAIN] PHOSPHATE.
CC -I- ENZYME REGULATION: POSSESSES AN AUTOINHIBITORY DOMAIN.
CC AUTOPHOSPHORYLATION APPEARS TO INCREASE THE ENZYMATIC ACTIVITY.
CC DOES NOT HAVE A CALMODULIN-BINDING DOMAIN.
```

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M66176; AB06337.1; -
 DR PIR: A40811; A40811.
 DR PIR: A37125; A37125.
 DR HSSP: Q63450; 1A06.
 DR Dictydb: DD01034; mlka.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation.
 FT DOMAIN 8 265 PROTEIN KINASE.
 FT NP_BIND 264 295 AUTONINIBITORY DOMAIN.
 FT BINDING 14 22 ATP (BY SIMILARITY).
 FT ACT_SITE 37 37 ATP (BY SIMILARITY).
 FT ACT_SITE 130 130 BY SIMILARITY.
 SQ SEQUENCE 295 AA; 33406 MW; 546CAED8F6ECD0B CRC64;

Query Match 15.3%; Score 498; DB 1; Length 295;
 Best Local Similarity 38.7%; Pred. No. 9.7e-20;
 Matches 111; Conservative 57; Mismatches 103; Indels 14; Gaps 7;

QY 172 YELGKGVGRGHGHTGSAVYKGGYK--GGTVAVKIATAKMTAISIEDVRRREVKILRA 229
 DB 8 YEFEEELGGRGAF-----SIYVLGENKQTKORAIKVINKSELGNDYE-KMLKMEVDILK 61

QY 230 LSGNNLVKRYDACEGDLNVIYMEICEGSELLDRILARGRTTEDEAKIAVQILSYVA 289
 DB 62 VN-HPNIIALKEFDTPPEKILYVMEVLTGSELDPKIVKESG-YSEDAANLVKRIYSAVG 119

QY 290 FCHLQGVVHDLKPENFLFTTRDENAPMKLIDFGLSDFIRPDERLNDIVSAYVVAPEVL 349
 DB 120 YLGLNIVHDLKPENFLFTTRDENAPMKLIDFGLSDFIRPDERLNDIVSAYVVAPEVL 179

QY 350 HRS-YSEADINSIGVITTYILLGSRPFARTESGIFRSVLRADPNEDDSPPPTVSAAEAK 408
 DB 180 NATGYDEKVDMSIGVITTYILLGSPFYGDYVEIFEQIMEANVEFPPEYMGISKEAK 239

QY 409 DFKVRFNLKDYRRKMTAVQALTHPMLRDEQRIPLDILFRILKOYL 455
 DB 240 DFIGKLIVYDVSKRLNATNANLHPMLKSNNSNNTIDTV--KKMEYI 283

RESULT 13
 KCQA_RAT
 ID KCQA_RAT STANDARD; PRT; 474 AA.
 AC P13234;
 DT 01-JAN-1990 (rel. 13, Created)
 DT 01-APR-1993 (rel. 25, Last sequence update)
 DT 20-APR-2001 (rel. 40, Last annotation update)
 DE CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN
 DE (EC 2.7.1.123) (CAM KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].
 GN CAMK4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-91288548; PubMed-1648230;
 RA Oimstede C. A., Bland M.M., Merrill B.M., Sahyoun N.;
 RT "Relationship of genes encoding Ca2+/calmodulin-dependent protein
 RT kinase Gr and calsperrin: a gene within a gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5784-5786(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91304387; PubMed-1649385;
 RA Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S.,
 RA Slaughter G.R., Ono T.;
 RT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
 RT cell-specific calmodulin-binding protein are derived from the same
 RT gene."
 RL Mol. Cell. Biol. 11:3960-3971(1991).
 RN [3]
 RP SEQUENCE OF 250-474 FROM N.A.
 RC STRAIN-SPRAGUE-DAMLEY; TISSUE-Brain;
 RX MEDLINE-89174647; PubMed-2538431;
 RA Oimstede C. A., Jensen K.F., Sahyoun N.;
 RT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
 RT granule cells. Identification of a novel neuronal
 RT calmodulin-dependent protein kinase."
 RL J. Biol. Chem. 264:5866-5875(1989).
 RN [4]
 RP SEQUENCE OF 306-474 FROM N.A., AND SEQUENCE OF 335-361.
 RC STRAIN-SPRAGUE-DAMLEY;
 RX MEDLINE-89123272; PubMed-2914893;
 RA Ono T., Slaughter G.R., Cook R.G., Means A.R.;
 RT "Molecular cloning sequence and distribution of rat calsperrin, a
 RT high affinity calmodulin-binding protein."
 RL J. Biol. Chem. 264:2081-2087(1989).
 CC -1- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
 CC ENRICHED IN CEREBELLAR GRANULE CELLS.
 CC -1- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
 CC PROTEIN.
 CC -1- CATALYTIC ACTIVITY: ATP + PROTEIN = ADP + O-PHOSPHOPROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
 CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
 CC SPLICING
 CC -1- TISSUE SPECIFICITY: CALSPERMIN IS PREDOMINANTLY FOUND IN MAMMALIAN
 CC TESTIS AND BRAIN.
 CC -1- PTM: THE N-TERMINAL OF CALSPERMIN IS BLOCKED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M63334; AAA40865.1; -
 DR EMBL: M74488; AAA40845.1; ALT_SEQ.
 DR EMBL: M64757; AAA40856.1; -
 DR EMBL: M64757; AAA40857.1; -
 DR EMBL: J04600; AAA41867.1; -
 DR EMBL: J04446; AAA40990.1; -
 DR PIR: A41103; TVRICA.
 DR HSSP: Q63450; 1A06.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Calmodulin-binding; Testis; Alternative splicing.
 FT CHAIN 306 474 CALSPERMIN.
 FT DOMAIN 42 296 PROTEIN KINASE.

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FT NP_BIND 48 56 ATP (BY SIMILARITY).
FT BINDING 71 71 ATP (BY SIMILARITY).
FT ACT_SITE 160 160 BY SIMILARITY.
FT DOMAIN 318 337 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 393 399 POLY-GLU.
FT DOMAIN 403 413 POLY-GLU.
FT CONFLICT 372 372 I -> M (IN REF. 2 AND 4);
SQ SEQUENCE 474 AA; 53133 MW; 56F71AC5644DED23 CRC64;

Query Match 15.2%; Score 495; DB 1; Length 474;
Best Local Similarity 35.6%; Pred. No. 2.4e-19;
Matches 119; Conservative 57; Mismatches 110; Indels 48; Gaps 11;

OY 105 PPPSPFAHKTATLAKLGGCKPKEGTPEEGVGAGGGGAGCAAGAEPRDLTKTFCF 164
DB 7 PSCPSPSCSSVSS-----TENLVDPDY-----IDSKRD-PLSPFF-- 42
OY 165 SKNFGAKYELGKREVGHGHGHTCSAVYKKGKYG--QTVAVKLIAMAKMTAISIEDVR 222
DB 43 -----EVESLGRG-----ATSIYRCOKGQKPYALKVKK-----TVDKKIVRT 84
OY 223 EKKILALSGHNNLVKFTACEDGLNVIYVMECEGELLRLANGKRTEDAKAIYV 282
DB 85 EGVGLRLTS-HPNITLKEIFETPTREISVLLELVGTGELFDRIVER-GYYSERDADAVK 142
OY 283 QILSVAFCHLOGVVRDLKPENFLETTDENAPMKLIDFGSLDFLRPERLNDIVGSAY 342
DB 143 QILEAVAYIHENIYHRDLKPENLATAPADPKLADGSKIVYEHQVLMKTVCGTTCG 202
OY 343 YVAEVLNR-SYSMEADINSIGVITYILLGSRHPV-ARTESGIFRSVLADPNFDSFP 400
DB 203 YCAPELRBCAAGPEVDNMSVGIITYILLGFEFPYDEKGDQMFRLNCEYFISPMW 262
OY 401 PIVSAEAKDFVKRFLNKDYRKMTAVOALTHPVL 434
DB 263 DEVSLNAKDLVKLIVLDPKRKLTFEQLQHPMV 296

RESULT 14
KCC1_YEAST STANDARD; PRT; 446 AA.
AC P27466;
AT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE CALTUM/CALMODULIN-DEPENDENT PROTEIN KINASE I (EC 2.7.1.123).
GN CMK1 OR YER014C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-91224102; PubMed-2026147;
RA Pausch M.H., Kaim D., Kunisawa R., Admon A., Thorner J.;
RT "Multiple Ca2+/calmodulin-dependent protein kinase genes in a
RT unicellular eukaryote."
RL EMBO J. 10:1511-1522(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-91286319; PubMed-2061341;
RA Ohya Y., Kawasaki H., Suzuki K., Londesborough J., Anraku Y.;
RT "Two yeast genes encoding calmodulin-dependent protein kinases.
RT Isolation, sequencing and bacterial expressions of CMK1 and CMK2."
RL J. Biol. Chem. 266:12784-12794(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RA MEDLINE-95400292; PubMed-7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasakuma S.-I., Sasakuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;

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RT RT Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae."
RL Nat. Genet. 10:261-268(1995).
CC -I- FUNCTION: IMPORTANT IN CELLULAR REGULATION.
CC -I- CATALYTIC ACTIVITY: ATP + A PROTEIN -> ADP + A PHOSPHOPROTEIN.
CC -I- SUBUNIT: MULTIMERIC.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CMK SUBFAMILY.
CC -----
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CC -----
DR EMBL; X57782; CAA0928.1; -
DR EMBL; D90375; BAA14383.1; -
DR EMBL; D50617; BAA09253.1; -
DR EMBL; D44599; BAA08031.1; -
DR PIR; A40896; A40896.
DR PIR; S16883; S16883.
DR HSSP; Q63450; IAO6.
DR SGD; S0001910; CMK1.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_kin_actsite.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Multigene family.
FT DOMAIN 37 299
FT NP_BIND 43 51 ATP (BY SIMILARITY).
FT BINDING 66 66 ATP (BY SIMILARITY).
FT ACT_SITE 161 161 BY SIMILARITY.
FT DOMAIN 312 323 CALMODULIN-BINDING (BY SIMILARITY).
FT CONFLICT 53 54 OA -> VR (IN REF. 1).
FT CONFLICT 68 68 L -> V (IN REF. 1).
FT CONFLICT 188 188 R -> T (IN REF. 1).
FT CONFLICT 199 202 PAGES -> AGTA (IN REF. 1).
FT CONFLICT 237 243 SAFRAER -> ATIDRK (IN REF. 1).
FT CONFLICT 271 271 K -> Q (IN REF. 1).
SQ SEQUENCE 446 AA; 50296 MW; 586C31CEDB311555 CRC64;

Query Match 15.1%; Score 493.5; DB 1; Length 446;
Best Local Similarity 37.6%; Pred. No. 2.6e-19;
Matches 135; Conservative 46; Mismatches 123; Indels 55; Gaps 11;

OY 171 KYELGKEVGHGHGHTCSAVK--KGEYKQTYAVAKI-IKAKMTAISIEDVREYKIL 227
DB 36 KYVEGKTLGAGTGG-----VVRQAKNTGDEDAVAILIKKAKGNKVOLEALYDELDIL 90
OY 228 RALSGHNNLVKFTACEDGLNVIYVMECEGELLRLANGKRTEDAKAIYOILSV 287
DB 91 QRLH-HPNIAFKDWFESKSKFYITQLAKGELFDRILK-GKTFEDAVRLIVELSLA 148
OY 288 VAFCHLOGVVRDLKPENFLETTDENAPMKLIDFGSLDFLRPER-LNDIVGSAYVAP 346
DB 149 VKVMHSGNVIYHRDLKPENLITIDKSDPSPLVADFGIAKRLKSDDELLYPAGSLGVAP 208
OY 347 EVLNR-SYSMEADINSIGVITYILLGSRFPV-RTESGIFRSVLADP-NEDDSRPPTY 403
DB 209 EVLTDGCHGRPCDIWSIGVITYILLGYSFAFRAERODFLDECTGEPVFRHPWDSV 268
OY 404 SAEAKDFVKRFLNKDYRKMTAVOALTHPVL-----RDEQR 439
DB 269 SNKAKQFIKALNLDPSKRTAAELLEDPMWICTELKTHNLGLKGLDAROKFRNSVE 328
OY 440 QIPDLILIFRLIKOYLRTAT-----PLKRLALAKLSKALREDELLYLK 481

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DB 329 RVLNKKIKRLDYLEQTESDSDFEQSQANGSVPLKATPTLSKSKSEEGSKLK 387
RESUL 15
KCC4_HUMAN STANDARD: PRT; 473 AA.
AC 016566;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN
DE (EC 2.7.1.123) [CAM KINASE-GR] [CONTAINS: CALSPERMIN].
CN CAMK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94375404; PubMed=8089075;
RA Klean T., Okuno S., Fujisawa H.;
RT "cDNA cloning and expression of human calmodulin-dependent protein
RT kinase IV."
RL J. Biochem. 115:637-640(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum, and Thymus;
RX MEDLINE=94252566; PubMed=8194751;
RA Bland M.M., Monroe R.S., Ohmsted C.A.;
RT "The cDNA sequence and characterization of the
RT Ca2+/calmodulin-dependent protein kinase-Gr from human brain and
RT thymus."
RL Gene 142:191-197(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94149862; PubMed=8107230;
RA Mosallos G., Hanissian S.H., Jawahar S., Vara L., Kleff E.,
RA Chaitia T.A.;
RT "A Ca2+/calmodulin-dependent protein kinase, Cam kinase-Gr, expressed
RT after transformation of primary human B lymphocytes by Epstein-Barr
RT virus (EBV) is induced by the EBV oncogene LMP1."
RL J. Virol. 68:1697-1705(1994).
CC -1- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC PROTEIN.
CC -1- CATALYTIC ACTIVITY: ATP + PROTEIN - ADP + O-PHOSPHOPROTEIN.
CC -1- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
CC NUCLEI (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
CC SPLICING.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
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CC -----
DR EMBL: D30742; BAA06403.1;
DR EMBL: L17000; AAA35639.1;
DR EMBL: L24959; AAA18251.1;
DR HSSP: Q63450; 1A06.
DR MIM: 114080;
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding; Alternative splicing.
FT CHAIN 310 473
FT DOMAIN 46 300 CALSPERMIN.
FT NP_BIND 52 60 ATP (BY SIMILARITY).
FT BINDING 75 75 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT DOMAIN 322 341 CALMODULIN-BINDING (POTENTIAL).
SQ SEQUENCE 473 AA; 51925 MW; EFEE51E5612326DC CRC64;

Query Match 15.0%; Score 490; DB 1; Length 473;
Best Local Similarity 40.1%; Pred. No. 4.3e-19;
Matches 107; Conservative 51; Mismatches 93; Indels 16; Gaps 7;

QY 172 YELGKEYGRGHFGHTGSAVYKKGKBYG--QTAVKIIAKAKMTAISIEDVREVKILRA 229
DB 46 FEVESELRG-----ATSIYRKOKGTOKPVALKVKR---TVDKKIVRTIEIGVLLR 95
QY 230 LSGHNILVKPYDACEGLNVIYVMECEGGLDRLILARGRYTEBDAAKAIYQILSYVA 289
DB 96 LS-HPNIIKKKEIFETPTETISLVLELVGTGELFDRIYK-GYSESDADAVKQILLEAVA 153
QY 290 FCHLOGVYHRDLKPENFLFTTRDENAPMKLIDGLSDFTRPDERLNDIVGSAVYVAPEVL 349
DB 154 YLHENGIVHRDLKPEMLVATPAPAPLKIADGLSKYIEHOVLKMTYCGTGYCAPETL 213
QY 350 HR-SYMEADIMSIGVITVYLLCGSRPFV-ARTESGIFRSVLRADNPFDSMPRTVSAA 407
DB 214 RCGAYGPEYDMSVGIITVILLOGFEPEFDERDQMFRRILNCEYFISPMWDEVSLNA 273
QY 408 KDFVKKFLNKDKRKRMTAVQALTHPWL 434
DB 274 KDLVRLIYLDPRKRLITFEALQHPWV 300

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Search completed: May 2, 2002, 08:49:46
Job time: 565 sec

Thu May 2 11:46:28 2002

us-09-854-731-4.rsp

Page 13

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2002, 08:37:31 ; Search time 122.34 Seconds
(without alignments)
744.872 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260
Sequence: 1 MGOCYKGCASGRTADDEGV.....LGFTKFLHGVTIRGSTRRH 623

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1 | 2862 | 87.8 | 625 | 10 | P93520 |
| 2 | 2831 | 86.8 | 607 | 10 | Q41792 |
| 3 | 2817 | 86.4 | 607 | 10 | Q9FYU0 |
| 4 | 2815.5 | 86.4 | 599 | 10 | Q41791 |
| 5 | 2251 | 66.0 | 452 | 10 | Q23797 |
| 6 | 2179 | 66.8 | 595 | 10 | Q9ZU22 |
| 7 | 1970 | 60.4 | 594 | 10 | Q9SG12 |
| 8 | 1948.5 | 59.8 | 594 | 10 | Q9FIM9 |
| 9 | 1917 | 58.6 | 601 | 10 | Q9SCS2 |
| 10 | 1911 | 58.6 | 601 | 10 | Q04290 |
| 11 | 1829 | 56.1 | 577 | 10 | Q9LET1 |
| 12 | 1816.5 | 55.7 | 576 | 10 | Q08673 |
| 13 | 1760.5 | 54.0 | 606 | 10 | Q9FX86 |
| 14 | 1749.5 | 53.7 | 415 | 10 | Q81088 |
| 15 | 1736.5 | 53.3 | 594 | 10 | Q9XGW6 |
| 16 | 1736.5 | 53.3 | 599 | 10 | Q9JLJ9 |
| 17 | 1576 | 48.3 | 459 | 10 | Q9XP48 |
| 18 | 1153.5 | 35.4 | 571 | 10 | Q48827 |
| 19 | 1106.5 | 33.9 | 523 | 10 | Q9SE25 |

| | | | | | |
|----|--------|------|-----|----|--------|
| 20 | 1080.5 | 33.1 | 512 | 10 | Q9SE24 |
| 21 | 1080 | 33.1 | 536 | 10 | Q65644 |
| 22 | 1072.5 | 32.9 | 523 | 10 | Q9FKW4 |
| 23 | 1039.5 | 31.9 | 564 | 10 | Q9ZTU9 |
| 24 | 926 | 28.4 | 528 | 10 | Q9FMP5 |
| 25 | 923.5 | 28.3 | 593 | 10 | Q9ZV15 |
| 26 | 905.5 | 27.8 | 518 | 10 | Q9AXA7 |
| 27 | 903.5 | 27.7 | 529 | 10 | Q42479 |
| 28 | 895.5 | 27.5 | 548 | 10 | Q9S7Z4 |
| 29 | 895.5 | 27.5 | 573 | 10 | P93838 |
| 30 | 889.5 | 27.3 | 540 | 10 | Q81390 |
| 31 | 887.5 | 27.2 | 548 | 10 | Q9S786 |
| 32 | 887 | 27.2 | 534 | 10 | Q9ZPM0 |
| 33 | 886 | 27.2 | 531 | 10 | Q41790 |
| 34 | 886 | 27.2 | 554 | 10 | Q49717 |
| 35 | 883.5 | 27.1 | 639 | 10 | Q9ZSA2 |
| 36 | 874 | 26.8 | 980 | 10 | Q9LORA |
| 37 | 871.5 | 26.7 | 646 | 10 | Q38870 |
| 38 | 860 | 26.4 | 490 | 10 | Q42396 |
| 39 | 859.5 | 26.4 | 554 | 10 | Q04123 |
| 40 | 859.5 | 26.4 | 531 | 10 | Q9ZSA2 |
| 41 | 858.5 | 26.3 | 532 | 10 | Q9XER6 |
| 42 | 853.5 | 26.2 | 465 | 10 | Q41793 |
| 43 | 852.5 | 26.2 | 560 | 10 | Q9SCM0 |
| 44 | 851 | 26.1 | 541 | 10 | Q38868 |
| 45 | 848.5 | 26.0 | 553 | 10 | Q80700 |

ALIGNMENTS

RESULT 1
ID P93520 PRELIMINARY; PRT; 625 AA.
AC P93520;
DT 01-MAY-1997 (TREMURE1. 03, Created)
DT 01-MAY-1997 (TREMURE1. 03, Last sequence update)
DT 01-JUN-2001 (TREMURE1. 17, Last annotation update)
DE CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE HOMOLOGY/CAM KINASE
DE HOMOLOGY/CAM KINASE
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96236830; PubMed=8680305;
RA Lu Y.T., Hidaka H., Feldman L.J.;
RT *Characterization of a calcium/calmodulin-dependent protein kinase
RT homolog from maize roots showing light-regulated gravitropism.*;
RL Planta 199;18-24(1996).
CC 1-1 SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; S82324; ABA47181.1; -;
DR HSSP; P00518; IPHK.
DR Mendel; 13809; Zeama;1112;13809.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk.pkinase.
DR InterPro; IPR002290; Ser_thr_kin_actsite.
DR Pfam; PF00068; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 625 AA; 68789 MW; 00011D3F7484D0B8 CRC64;

Query Match 87.8%; Score 2862; DB 10; Length 625;
Best Local Similarity 87.7%; Pred. No. 2.5e-193;
Matches 561; Conservative 31; Indels 32; Gaps 7;
QY 1 MGOCYKGCASGRT--ADDEGVTEHQSPPPPANGLPSTPPRQQAQAQAVGTPTRR 55

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Db      1 MGOCYGRAGASSRRADHDADPSGASVAPSPPLPANGAPLP-----ATPRRH 47
QY      56 GSKSGSTTPGHO-----TPG-VAMPSPYSGASPLPAGVSPSPARSTPRRFFKRPSPPS 110
Db      48 --KSGSTTPVHHQAAAPGAAMPSPYPAGASPLPAGVSPSPARSTPRRFFKRPSPPS 105
QY      111 PAKIKRATLAKRLGGGPKRGKGTPEEGVGAGGGG-----GAADGAETERPLDKTEG 163
Db      106 PAKIKRATLAKRLGGGPKRGKGTPEEGVGAGAGAGAGAGAAVGAADSAEADRPDLKTEG 165
QY      164 FSNFNGAKVELKGVGRGHEGHTCSAVVKGEGQTVAVKIIAKAKMTAISIEDVRE 223
Db      166 FANFNGAKVDLKEVGRGHEGHTCSAVVKGEGHTVAVKIIAKAKMTAISIEDVRE 225
QY      224 VKILRALSGHNNLVKFFYDACEGLANYIYMWELCEGELLDRLLARGRYTEEDAKAIYVQ 283
Db      226 VKILKALSGHNNLVKFFYDACEGLANYIYMWELCEGELLDRLLARGRYTEEDAKAIYVQ 285
QY      284 ILSVAFCHLQGVVHRDLKPENFLFTTRDENAPMKLIDFGLSDFTRPDERLNDIVGSAVY 343
Db      286 ILSVAFCHLQGVVHRDLKPENFLFTTRDESAPMKLIDFGLSDFTRPDERLNDIVGSAVY 345
QY      344 VAPENVHRSYSMEADINSGVITTYILLGSRPPMARTESGIFRSVLRADPNFDSMPWPTV 403
Db      346 VAPENVHRSYSMEADINSGVITTYILLGSRPPMARTESGIFRSVLRADPNFDSMPWPSV 405
QY      404 SAEANDFVRFLNKDYRKRMATAVOALTHPWLDEOROLPLDILFRLKOYLKATPLKRL 463
Db      406 SAEANDFVRFLNKDYRKRMATAVOALTHPWLDEOROLPLDILFRLKOYLKATPLKRL 465
QY      464 ALKALSKALREDELLYLKLOFKLEPRDGVSLDNFRTALTRYLDAMKESRYLEFLHAL 523
Db      466 ALKALSKALSEDELLYLKLOFKLEPRDGVSLDNFRTALTRYLDAMKESRYLEFLHAL 525
QY      524 EPLAVRMDFEBCAAASIPYOLEALERWEELAGTAFQFDEGNRVISVELAOELNLA 583
Db      526 EPLAVRMDFEBCAAASIPYOLEALERWEELAGTAFQFDEGNRVISVELAOELNLA 585
QY      584 PTHYSIVODWIRKSDGKLNFLGTFKFLHGVITRGSNTRRH 623
Db      586 PTHYSIVODWIRKSDGKLNFLGTFKFLHGVITRGSNTRRH 625

RESULT 2
ID      041792      PRELIMINARY:      PRT:      607 AA.
AC      041792:
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      CDPK-RELATED PROTEIN KINASE.
OS      Zea mays (Maize).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC      Panicoideae; Andropogoneae; Zea.
OX      NCBI_TaxID=4577;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=IMBRED LINE H84; TISSUE=ROOT;
RX      MEDLINE=97072168; PubMed=8914977;
RA      Furumoto T., Ogawa N., Hata S., Izui K.;
RT      "Plant calcium-dependent protein kinase-related kinases (CRKS) do not
RT      require calcium for their activities.";
RL      FEBS Lett. 396:147-151(1996).
CC      -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR      EMBL: D84508; BAA12692.1;
DR      HSSP: P00518; 2PKH.
DR      Mendei: 13825; Zeam: 1112;13825.
DR      InterPro: IPR002048; EF-hand.
DR      InterPro: IPR000719; Euk.pkinase.
DR      InterPro: IPR002290; Ser_thr_kin_actsite.
DR      Pfam: PF00069; pkinase; 1.

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DR      SMART: SM00220; S_TKC; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ      SEQUENCE 607 AA; 67397 MW; E9B646E1C197CC3B CRC64;

Query Match
Best Local Similarity 86.8%; Score 2831; DB 10; Length 607;
Matches 553; Conservative 18; Mismatches 33; Indels 22; Gaps 7;

QY      1 MGOCYGRAGASSRRADHDADVAP--PSPLPANGAP--TPGQPA-----TPGRR--K 47
Db      1 MGOCYGRAGASSRRADHDADVAP--PSPLPANGAP--TPGQPA-----TPGRR--K 47
QY      59 GSGTTP-CHQTPGVAMPSPYPSGASPLPAGVSPSPARSTPRRFFKRPSPPAKHKA 117
Db      48 GSGATPVHHQAAATPAMPSPYPAGASPLPAGVSPSPARSTPRRFFKRPSPPAKHKA 107
QY      118 TLAKRLGGGPKRGKGTPEEGVGAGGGGGAADGAETERPLDKTEGSKNFKATLKE 177
Db      108 TLAKRLGGGPKRGKGTPEEGVGAGGGGGAADGAETERPLDKTEGSKNFKATLKE 161
QY      178 VGRGHFHTCSAVVKGEGYQTVAVKIIAKAKMTAISIEDVRRREVKILKALSGHNNLV 237
Db      162 VGRGHFHTCSAVVKGEGYQTVAVKIIAKAKMTAISIEDVRRREVKILKALSGHNNLV 221
QY      238 KFYDACEDGLNYIYMWELCEGELLDRLLARGRYTEEDAKAIYVQIILSVAFCHLQGV 297
Db      222 KFYDACEDGLNYIYMWELCEGELLDRLLARGRYTEEDAKAIYVQIILSVAFCHLQGV 281
QY      298 HRDLKPENFLFTTRDENAPMKLIDFGLSDFTRPDERLNDIVGSAVYVAPENVHRSYSME 357
Db      282 HRDLKPENFLFTTRDESAPMKLIDFGLSDFTRPDERLNDIVGSAVYVAPENVHRSYSME 341
QY      358 DIVSIGVITTYILLGSRPPMARTESGIFRSVLRADPNFDSMPWPSVSAEAKDFVRFLNK 417
Db      342 DIVSIGVITTYILLGSRPPMARTESGIFRSVLRADPNFDSMPWPSVSAEAKDFVRFLNK 401
QY      418 DYKRMATAVOALTHPWLDEOROLPLDILFRLKOYLKATPLKRLALKALSKALREDEL 477
Db      402 DYKRMATAVOALTHPWLDEOROLPLDILFRLKOYLKATPLKRLALKALSKALREDEL 461
QY      478 LYKLOFKLEPRDGVSLDNFRTALTRYLDAMKESRYLEFLHALLEPLAVRMDFEBC 537
Db      462 LYKLOFKLEPRDGVSLDNFRTALTRYLDAMKESRYLEFLHALLEPLAVRMDFEBC 521
QY      538 AAASIPYOLEALERWEELAGTAFQFDEGNRVISVELAOELNLAPTHYSIVODWIRKS 597
Db      522 AAASIPYOLEALERWEELAGTAFQFDEGNRVISVELAOELNLAPTHYSIVODWIRKS 581
QY      598 DCKLNFLGTFKFLHGVITRGSNTRRH 623
Db      582 DCKLNFLGTFKFLHGVITRGSNTRRH 607

RESULT 3
ID      09FYUO      PRELIMINARY:      PRT:      607 AA.
AC      09FYUO:
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      CALCIUM/CALMODULIN DEPENDENT PROTEIN KINASE MCK2.
OS      Zea mays (Maize).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC      Panicoideae; Andropogoneae; Zea.
OX      NCBI_TaxID=4577;
RN      [1]
RP      SEQUENCE FROM N.A.

```

RA Lu Y.-T., Liang S., Wang L.;
 RT "Cloning of a calcium/calmodulin-dependent protein kinase gene, MCK2
 from maize."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289237; MAG01179.1; -
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR SMART: SM00219; TyKc.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; Transferase.
 KM
 SQ SEQUENCE 607 AA; 67521 MW; 8907CD0F4DEC3810 CRC64;

Query Match 86.4%; Score 2817; DB 10; Length 607;
 Best Local Similarity 87.9%; Pred. No. 3.6e-190;
 Matches 550; Conservative 20; Mismatches 34; Indels 22; Gaps 7;

QY 1 MGQCYGR--GASGRADDEGVYEHOSPPRANGLPSTPPRQQAQAQVGTTRRRGSK 58
 DB 1 MGQCYGRAGGASSRRADHDVAP--PSPRPANGAP--TPPOQA-----TGR--K 47
 QY 59 SGSTTP-GHOTPGVAMPSPYSGASPLPAGVSPSPARSTRRFRFPSPPAKHKA 117
 DB 48 SGSTTPVNHQAATTAMPSPYAGASPLPAGVSPSPARSTRRFRFPSPPAKHKA 107
 QY 118 TLARLGGKREKGTPEEGVGAGGGGGAADAEETPLDKTFGSKNGAYELKE 177
 DB 108 TLARLGGKREKGTPEEGGAGV-----AADSAAERPLDKTFGSKNGAYELKE 161
 QY 178 VGRHGHGHTSAVVKKEGKQGVAVKTIKAKMTTASIEDVREVKIILALSGHNLY 237
 DB 162 VGRHGHGHTSALVKKGVKHAVALKISAKMTTASIEDVREVKIILALSGHNLY 221
 QY 238 KFYDACEGDLNVYIMELCEGELLDRILANGRYTEEDAKAIYVOILSVAFCHLGCV 297
 DB 222 KFYDACEGDLNVYIMELCEGELLDRILANGRYTEEDAKAIYVOILSVAFCHLGCV 281
 QY 298 HRDLKPENFLFTTIDENAPMKLIDFGLSDTIRPDERLNDIVGSAVYVAEVLHRSYMEA 357
 DB 282 HRDLKPENFLFTTIDENAPMKLIDFGLSDTIRPDERLNDIVGSAVYVAEVLHRSYMEA 341
 QY 358 DIMSIGVITTYLLCGSRPFMAKTESGIFRSVLRADPNFDDSPWTVSAEADFYKRFYLNK 417
 DB 342 DIMSIGVITTYLLCGSRPFMAKTESGIFRSVLRADPNFDDSPWTVSAEADFYKRFYLNK 401
 QY 418 DYRRKMTAVQALTRPMLRDEQROIPLDILIFRLIKOYLRAPIPLKRLAKLSKALREDEL 477
 DB 402 DYRRKMTAVQALTRPMLRDEQROIPLDILIFRLIKOYLRAPIPLKRLAKLSKALREDEL 461
 QY 478 LYLKLFQKLEPRRGFVSLDNFRALTRYLTDAMKESVLEFLALREPLAYRRMDEEFC 537
 DB 462 LYLKLFQKLEPRRGFVSLDNFRALTRYLTDAMKESVLEFLALREPLAYRRMDEEFC 521
 QY 538 AAATSPVQLEALRMEETAGTAFOOFBOEGNRVTSVEELAOELNAPHYSTVODMIRKS 597
 DB 522 AAATSPVQLEALRMEETAGTAFOOFBOEGNRVTSVEELAOELNAPHYSTVODMIRKS 581
 QY 598 DGKLNFLGTFKFLHGVITRGSNTRRH 623
 DB 582 DGKLNFLGTFKFLHGVITRGSNTRRH 607

RESULT 4
 ID 041791 PRELIMINARY; PRT; 599 AA.
 AC 041791;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CDPK-RELATED PROTEIN KINASE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC clade;
 OC Panicoidae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=INBRED LINE H84; TISSUE=ROOT;
 RX MEDLINE=97072168; PubMed=8914977;
 RA Furumoto T., Ogawa N., Hata S., Izui K.;
 RT "Plant calcium-dependent protein kinase-related kinases (CRKs) do not
 require calcium for their activities."
 RL FEBS Lett. 396:147-151(1996).
 CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: D84507; BAI12691.1; -
 DR HSSP: P00518; IPRK.
 DR Mendel; 13824; Zeama; 1112; 13824.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00069; pkinase.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 FT
 SQ SEQUENCE 599 AA; 66212 MW; ADF6193D37B51BFC CRC64;

Query Match 86.4%; Score 2815.5; DB 10; Length 599;
 Best Local Similarity 89.4%; Pred. No. 4.3e-190;
 Matches 547; Conservative 16; Mismatches 20; Indels 29; Gaps 5;

QY 26 SPPRANGLPSTPPRQQAQAQVGTTRRRGSKSGSTTPGHQ---TPG-VAMSPYPSG 80
 DB 3 SPLRANGAPLP-----ATPRRH--KSSSTTPVNHQAATTGAAMASPYRAG 47
 QY 81 GASPLPAGVSPSPARSTRRFRFPSPPAKHKATLAKRLGGKREKGTPEEGVG 140
 DB 48 GASPLPAGVSPSPARSTRRFRFPSPPAKHKATLAKRLGGKREKGTPEEGVG 107
 QY 141 AGGGG-----GAADGAETPLDKTFGSKNGAYELKEVGRGHGHTCSAVV 191
 DB 108 AGAGAGAGAGAAVGAADSAEADRPDKTFGFAKNFGAKYDLGKEVGRGHGHTCSAVV 167
 QY 192 KGEYKGTAVVKTIKAKMTTASIEDVREVKIILALSGHNLYKFYDACEGDLNVYI 251
 DB 168 KGEYKGTAVVKTIKAKMTTASIEDVREVKIILALSGHNLYKFYDACEGDLNVYI 227
 QY 252 VMEICEGELLDRILANGRYTEEDAKAIYVOILSVAFCHLGCVYHRDLKPENFLPTR 311
 DB 228 VMEICEGELLDRILANGRYTEEDAKAIYVOILSVAFCHLGCVYHRDLKPENFLPTR 287
 QY 312 DENAPMKLIDFGLSDTIRPDERLNDIVGSAVYVAEVLHRSYMEADIMSIGVITYILLC 371
 DB 288 DENAPMKLIDFGLSDTIRPDERLNDIVGSAVYVAEVLHRSYMEADIMSIGVITYILLC 347
 QY 372 GSRRPFMAKTESGIFRSVLRADPNFDDSPWTVSAEADFYKRFYLNKDKRMTAVQALTH 431
 DB 348 GSRRPFMAKTESGIFRSVLRADPNFDDSPWTVSAEADFYKRFYLNKDKRMTAVQALTH 407
 QY 432 PWLRDEQROIPLDILIFRLIKOYLRAPIPLKRLAKLSKALREDELTLKLFQKLEPRD 491
 DB 408 PWLRDEQROIPLDILIFRLIKOYLRAPIPLKRLAKLSKALREDELTLKLFQKLEPRD 467
 QY 492 GFVSLDNFRALTRYLTDAMKESVLEFLALREPLAYRRMDEECCAATSPVQLEALER 551
 DB 468 GFVSLDNFRALTRYLTDAMKESVLEFLALREPLAYRRMDEECCAATSPVQLEALER 527

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QY 552 WEELAGTAFOOFEQGNRVISVEELAOELNAPTHYSIVODWIRKSDGKLNFGTRKELH 611
DB 528 WEELAGTAFOHFEQGNRVISVEELAOELNAPTHYSIVODWIRKSDGKLNFGTRKELH 587
QY 612 CVTIRGSNTRRH 623
DB 588 GVTIRGSNTRRH 599

RESULT 5
023797
ID 023797 PRELIMINARY; PRT; 452 AA.
AC 023797;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALCIUM-DEPENDENT PROTEIN KINASE-RELATED KINASE (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INBERD LINE H84; TISSUE=LEAF;
RX MEDLINE=97072168; PUBMED=8914977;
RA Furumoto T., Ogawa N., Hata S., Izui K.;
RT "Plant calcium-dependent protein kinase-related kinases (CRKS) do not
RT require calcium for their activities.";
RL FEBS Lett. 396:147-151(1996).
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: D38452; BAA22410.1; -.
DR HSSP: P00518; 1PKH.
DR Mendel: 24438; Zeama:1112;24438.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT NON-TER
SQ SEQUENCE 452 AA; 51789 MW; 42C3A5A76A3053P4 CRC64;

Query Match 69.0%; Score 2251; DB 10; Length 452;
Best Local Similarity 95.6%; Pred. No. 1.7e-150;
Matches 432; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

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QY 472 LREDELLYKLOFKLEPRDGVSLDNFRTALRYLTDAMKESRYLEFLHALPLATYRRM 531
DB 301 LSEDELLYRLOPKLEPRDGVSLDNFRTALRYLTDAMKESRYLEFLHALPLATYRRM 360
QY 532 DFEFCAAAIISPYOLEALERMEELAGTAFOOFEQGNRVISVEELAOELNAPTHYSIVO 591
DB 361 DFEFCAAAIISPYOLEALERMEELAGTAFOHFEQGNRVISVEELAOELNAPTHYSIVO 420
QY 592 DWIRKSDGKLNFGTRKELHGVITIRGSNTRRH 623
DB 421 DWIRKSDGKLNFGTRKELHGVITIRGSNTRRH 452

RESULT 6
09ZU22
ID 09ZU22 PRELIMINARY; PRT; 595 AA.
AC 09ZU22;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE HYPOTHETICAL 66.6 KDA PROTEIN.
GN T3A4.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Rongning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: TO EF-HAND FAMILY.
DR EMBL: AC005819; AAC69927.1; -.
DR HSSP: P24941; 1CKP.
DR Mendel: 34144; Arabid.1112;34144.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00036; efhand; 1.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Calcium-binding; Hypothetical protein;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 595 AA; 66599 MW; C6D9C158BBA41A39C CRC64;

Query Match 66.8%; Score 2179; DB 10; Length 595;
Best Local Similarity 68.3%; Pred. No. 3e-145;
Matches 426; Conservative 71; Mismatches 93; Indels 34; Gaps 7;

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|--------|---|--|-----|
| QY | 239 | FYDACEDGLANTYIWMELCEGEGELLDRITLARGRYTEEDAKAIYQIILSVAFCHLQGVH | 298 |
| QY | 239 | | 298 |
| Db | 210 | YVDACEDANNVYIMELCDGSELLDRILARGKIPEDDARAIVQIILTVSFCHLQGVH | 265 |
| QY | 299 | RDLRPFENFLFTTRDENAMPKLIDFGLSDFIRPDERLNDIVGSAYVAPEVLRHSYMEAD | 356 |
| Db | 270 | RDLRPFENFLFTSSRSDSLKILDEGLSDFIRPDERLNDIVGSAYVAPEVLRHSYSLEAD | 322 |
| QY | 359 | IMSGIVITVYIILCCSRPPMATTEGSIIPRSVLRAPNPDSDSWPVSLEADPFVKRFLNKD | 418 |
| Db | 330 | IMSGIVITVYIILCCSRPPMATTEGSIIPRSVLRAPNPDSDSWPVSLEADPFVKRFLNKD | 389 |
| QY | 419 | YRKRMATAVQALTHWMLRPEORQIPDLIIIFPLIKOYLRATPKRLAKLAKLSKALREDEL | 478 |
| Db | 390 | YRKRMASNAQALTHWMLRNDSDSVIFLIDILITVLRVAYLHAPLRRAALKALAKALTEDELV | 449 |
| QY | 479 | YLIKQIFLLER-RDGFVSLDNFRATRYLTDMAKESRYVEELHLEPLAYRRMDFEEFC | 537 |
| Db | 450 | YLRQPFMLIGNKDGSVSLFNFKTALQMNATDAMRESVPFELITHTMESLRKMYFEEFC | 509 |
| QY | 538 | AAASIPYQLELHERRETAGTAFOFQEOEGKRVISVEELAQELMLATPHYSIVQDWIRKS | 597 |
| Db | 510 | AAASIHOLEAVDAWEELATATGFOHFETEGKRVITTEELARELNVGASNGHLDWVRSS | 565 |
| QY | 598 | DGKLNELGFTKFLHGVTIRGSNTR 621 | |
| Db | 570 | DGKLSYLGFTKFLHGVTILRAAHAR 593 | |
| RESULT | 7 | | |
| QY | 09SG12 | PRELIMINARY; PRT; 594 AA. | |
| AC | 09SG12; | | |
| DT | 01-MAY-2000 (Tremblrel_13, Created) | | |
| DT | 01-MAY-2000 (Tremblrel_13, Last sequence update) | | |
| DT | 01-JUN-2001 (Tremblrel_17, Last annotation update) | | |
| DE | POTATIVE CALCIUM DEPENDENT PROTEIN KINASE. | | |
| GN | TIG12.7 OR F2K15.230. | | |
| OS | Arabidopsis thaliana (Mouse-ear cress). | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | |
| OC | Eucosids II; Brassicales; Brassicaceae; Arabidopsis. | | |
| OX | NCBI_TaxID=3702; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=CV, COLUMBIA; | | |
| RA | Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D., | | |
| RA | Maiti R., Roning C.M., Koo H., Fujii C.Y., Uterback T.R., | | |
| RA | Barnstead M.E., Bowman C.L., White O., Nieman W.C., Fraser C.M., | | |
| RT | 'Arabidopsis thaliana chromosome 1 BAC TIG12 genomic sequence.'; | | |
| RL | Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases. | | |
| RP | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Rieger M., Gebel C., Mueller-Auer S., Schaefer M., Zipp M., | | |
| RA | Mewes H.W., Lemke K., Mayer K.F.X., Quelier F., Salanoubat M.; | | |
| RL | Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases. | | |
| CC | -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES. | | |
| DR | EMBL; AC012329; AAG5216.1; - | | |
| DR | EMBL; AL132956; CAB66416.1; - | | |
| DR | HSSP; Q63450; 1A06. | | |
| DR | InterPro; IPR000719; Euk_Pkinase. | | |
| DR | InterPro; IPR002290; Ser_thr_kin_actsite. | | |
| DR | SMART; SM00220; S_TKc; 1. | | |
| DR | PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1. | | |
| DR | PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. | | |
| DR | PROSITE; PS00108; PROTEIN_KINASE_ST; 1. | | |
| KW | ATP-binding; kinase; serine/threonine-protein kinase; transferase. | | |
| SO | SEQUENCE 594 AA; 66371 MW; 28170246FB708F59 CRC64; | | |

Query Match 60.4%; Score 1970; DB 10; Length 594;

| QY | 1 | MGCCYKGCASRTADDEGGVYTEHOSPPRANGLSTPPRQQAQAQVQVTPRRRGSG | 60 |
|--------|---|---|-----|
| Db | 1 | MGHCYSRNIISTVDDDE-----IP\$-----ATAQLPHRSOHNHQTSSS | 39 |
| QY | 61 | STTPHCHQPCVAMSPSPY-SSGASPLPAGVSPSPARSPRRFRKPPPPSPRAKIATKL | 119 |
| Db | 40 | SSIP--QSPAPSEVNPYIMISPPQSLPAGVAPSPAR-TPGRKFPPPPSPRAKIMAL | 96 |
| QY | 120 | AKRLG-GSKPKRGTPPEBGVAGAGGGGADGATEPRLDTKFGFSNFGAKYELGKEV | 178 |
| Db | 97 | RRRGTAAHPRDPGLPEPDESEAGSGGG-----ER-LDKNPFAPNBEKYELGKEV | 148 |
| QY | 179 | GRGHGHTCSAAYKKGKYGQTVAAVKIATAKMTAISIEDVRRREKYLIALSGHNILVK | 238 |
| Db | 149 | GRGHGHTCSMAKAKKGIKQGTVAVKIISKSMTSALSTIEDVRRREKYLIALSGSHNVK | 208 |
| QY | 239 | FYDACEDELNYYIWEELCEGGELDRILIARGRYTEEDAKALVQILSVAFCHLQGVH | 298 |
| Db | 209 | FYDVFEDSDNFFVWELCEGGELDSILARGRYEAAKRLVQILSATAFHLQGVH | 268 |
| QY | 299 | RLDKENELFTTRDENAPMKLIDFGLSPFIRPEDELNDIVGSAYVVAPEVLHRSYMEAD | 358 |
| Db | 269 | RLDKENELFTFSKNDAVLKVIDFELSDFARFDQALNDVGSAYVVAPEVLHRSYSTED | 328 |
| QY | 359 | IWSIGVITYILLCSRPFWARTESGIFRSVLRADPNFDDSPMPTVSAEAKDFVKRLNKD | 418 |
| Db | 329 | IWSIGVITYILLCSRPFGYRTESAIPFCVLRANPNFDLPMPSPISLAKDEVKRLNKD | 388 |
| QY | 419 | YRKRMATVQALTHPMLRDOROIPLDILIFRLIKOYLATPLKRLAKALSKALREDEL | 478 |
| Db | 389 | HRKRMATAQALAHPLRDENPGLIDFSGIYKVSYIRASPPRALKSLSKALEEELV | 448 |
| QY | 479 | YLKLOEFLLEPRDGVSLDNFRTALTRYLTLDPMKESRYLEFHLALEPLAYRRMDEEFCA | 538 |
| Db | 449 | FLKQFMLELPEPDGSLHLNFTLATRTATDMISRLPLDILNMQPLAKHLKDEEFCA | 508 |
| QY | 539 | AAISPYOLEALEMERELAGTAFQOEEOEGSNRYISVEELAQELNLAPTHYSIVQDMIRKSD | 598 |
| Db | 509 | ASVSYYOLEALEMEQIATVAFEPHESGSGRAISVQELAEEMSLGPNMYPLLKDMIRSD | 568 |
| QY | 599 | GKLNPLGFTKFLHGVTIRGSNTR 621 | |
| Db | 569 | GKLNPLGYAKFLHGVTIRSSSR 591 | |
| RESULT | 8 | | |
| Q9FIM9 | ID | Q9FIM9 PRELIMINARY; PRT; 594 AA. | |
| AC | Q9FIM9; | | |
| DT | 01-MAR-2001 (Tremblrel. 16, Created) | | |
| DT | 01-MAR-2001 (Tremblrel. 16, last sequence update) | | |
| DE | 01-JUN-2001 (Tremblrel. 17, last annotation update) | | |
| CC | CALCIUM DEPENDENT PROTEIN KINASE-LIKE PROTEIN. | | |
| OS | Arabidopsis thaliana (Mouse-ear cress). | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| CC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | |
| OC | eucosids II; Brassicales; Brassicaceae; Arabidopsids. | | |
| OX | NCBI_TaxID=3702; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN-COLUMBIA; | | |
| RX | MEDLINE=99156233; PubMed=10048488; | | |
| RA | Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N., | | |
| RA | Tabata S.; | | |
| RT | "Structural analysis of Arabidopsis thaliana chromosome 5. VIII. | | |
| RT | Sequence features of the regions of 1,081,958 bp covered by seventeen | | |
| RL | physically assigned pl and TAC clones."; | | |
| RL | DNA Res. 5:379-391(1998). | | |
| DR | EMBL; AB016884; BAB11236.1; - | | |
| DR | EMBL; AB025641; BAB11236.1; JOINED. | | |

DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actstite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00069; pkinase.1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; transferase.
 KW SEQUENCE 594 AA; 66514 MW; 01E00D979D4A441 CRC64;

Query Match 59.8%; Score 1948.5; DB 10; Length 594;
 Best Local Similarity 62.8%; Pred. No. 5.1e-129;
 Matches 392; Conservative 80; Mismatches 117; Indels 35; Gaps 11;

QY 1 MGCCYKASGRTADDEGGVYTHQSPRANGLPSTPPQQAQAAQVGTERRGSKG 60
 DB 1 MGHCYSNNTSA-VEDE-----IPGNGEVSNQPSQ---NHRHASIPQ---SPVA 43
 QY 61 STTPGHQTPGVAMPSPYPSGASPLPAGVSPSPARSTPRFRKRPSPPAKHITATLA 120
 DB 44 SGPEVNSYNI---SPF-----QSPPLPAGVAPSPAR-TPERKRPKPPPPSPAKPIAALR 95
 QY 121 KRLGG-CKREGTPE--BGVAGAGGGGAADGAETERPDKTGFSGKNGAKYELGKE 177
 DB 96 RRGAGAPQPPDEPIPEDSDVVDHGDGSGG-----ER-LDKNFGFGKNEGKYEELGKE 148
 QY 178 VGRHGHGHTCSAVKKGEGKQTVAVKTIKAKMTAISIEDVREKVITRLASHNNLV 237
 DB 149 VGRHGHGHTCSAKKAKKAKKAKKAKKAKKAKKAKKAKKAKKAKKAKKAKKAKKAKK 208
 QY 238 KRYDACEGLNAYIYWELEGGELLDRILANGRYTEEDAKAIYQIISVAACHLOGV 297
 DB 209 KRYDVEDADNVEYWELEGGELLDRILANGRYTEEDAKAIYQIISVAACHLOGV 268
 QY 298 HNDLKPENLFTTRDENAPMKLIDGLSDTRPRLNDIYGSAYYAEVLAHSYMEA 357
 DB 269 HNDLKPENLFTSRNEDALIKYIDGLSDTRPRLNDIYGSAYYAEVLAHSYSTEA 328
 QY 358 DWSIGVITTYLLCGSRPFWARTESGIRSVLRADPNFDDSPWPTVSAEAKDFKRLNK 417
 DB 329 DWSIGVITTYLLCGSRPFWARTESGIRSVLRADPNFDDSPWPTVSAEAKDFKRLNK 388
 QY 418 DYRKMTAVQALTHPMLDEQROIPDLILFRILKQYIRAPLRLAKLSKALREDEL 477
 DB 369 DYRKMTAVQALTHPMLDEQROIPDLILFRILKQYIRAPLRLAKLSKALREDEL 448
 QY 478 LYLKQFLLEPRDGFVSLDNFRTALTRYLTDAKESRVLEFLHALEPLAYRRRDEFEFC 537
 DB 449 VFLKQFLLEPRDGFVSLDNFRTALTRYLTDAKESRVLEFLHALEPLAYRRRDEFEFC 508
 QY 538 AAASIPYQLEALERMEELAGTAFOQFQEGNRYISVELAQLNLADTHYSIVQDWIRKS 597
 DB 509 AAASIPYQLEALERMEELAGTAFOQFQEGNRYISVELAQLNLADTHYSIVQDWIRKS 568
 QY 598 DGKLNFLGFTKFLHGVYIRGSNTR 621
 DB 569 DGKLNFLGFTKFLHGVYIRGSNTR 592

RESULT 9
 09SCS2 PRELIMINARY; PRT; 601 AA.
 AC 09SCS2;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DE CDPK-RELATED PROTEIN KINASE.
 GN T20E23.130.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID-3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Baynes M., Perez-Perez A., Terol J., Torres A., Perez-Alonso M.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X., Queller F., Salanoubat M.,
 RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL: AL133363; CAB62482.1; -
 DR HSSP: P00518; 1PK.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actstite.
 DR Pfam: PF00036; ehand; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Calcium-binding; Kinase; Serine/threonine-protein kinase;
 KW transferase.
 KW SEQUENCE 601 AA; 66991 MW; 61BA502B53C25DBF CRC64;

Query Match 58.8%; Score 1917; DB 10; Length 601;
 Best Local Similarity 60.4%; Pred. No. 8.5e-127;
 Matches 380; Conservative 87; Mismatches 116; Indels 46; Gaps 9;

QY 1 MGCCYKASGRTADDEGGVYTHQSPRANGLPSTPPQQAQAAQVGTERRGSKG 56
 DB 1 MGHCYSNNTSA-VEDE-----IPGNGEVSNQPSQ---NHRHASIPQ---SPVA 50
 QY 57 SKSG-----STTPGHQTPGVAMPSPYPSGASPLPAGVSPSPARSTPRFRKRPSPPAKH 111
 DB 51 KSPPEPFPSPSAHYFFSKKTPARSPANST-----NSTPKRFFFRPPPPSP 99
 QY 112 AKHITAKRLGGKPKEGTPEEGVGAGGGGAADGAETERPDKTGFSGKNGAK 171
 DB 100 AKHITAKRLGGKPKEGTPEEGVGAGGGGAADGAETERPDKTGFSGKNGAK 147
 QY 172 YELGKRVGCHGHTCSAVKKGEGKQTVAVKTIKAKMTAISIEDVREKVITRLALS 231
 DB 148 YELGKRVGCHGHTCSAVKKGEGKQTVAVKTIKAKMTAISIEDVREKVITRLALS 207
 QY 232 GHNILVRFYDACEGLNAYIYWELEGGELLDRILANGRYTEEDAKAIYQIISVAFC 291
 DB 208 GHNILVRFYDACEGLNAYIYWELEGGELLDRILANGRYTEEDAKAIYQIISVAFC 267
 QY 292 HQGVVHRLAKENLFTTRDENAPMKLIDGLSDFIRPDERLNDIYGSAYYAEVLAHR 351
 DB 268 HQGVVHRLAKENLFTTRDENAPMKLIDGLSDFIRPDERLNDIYGSAYYAEVLAHR 327
 QY 352 SYSMEADISIGVITTYLLCGSRPFWARTESGIRSVLRADPNFDDSPWPTVSAEAKDF 411
 DB 328 SYSMEADISIGVITTYLLCGSRPFWARTESGIRSVLRADPNFDDSPWPTVSAEAKDF 387
 QY 412 KRLNKDYRKMTAVQALTHPMLRD-EQROIPLDILFRILKQYIRAPLRLAKLSKAL 470
 DB 388 KRLNKDYRKMTAVQALTHPMLRD-EQROIPLDILFRILKQYIRAPLRLAKLSKAL 447
 QY 471 ALREDELTYLQFLLEPR-RDGFVSLDNFRTALTRYLTDAKESRVLEFLHALEPLAYR 529
 DB 448 ALREDELTYLQFLLEPR-RDGFVSLDNFRTALTRYLTDAKESRVLEFLHALEPLAYR 507
 QY 530 RMDPEEFCAALISVQLEALERMEELAGTAFOQFQEGNRYISVELAQLNLADTHYSIV 587
 DB 508 RMDPEEFCAALISVQLEALERMEELAGTAFOQFQEGNRYISVELAQLNLADTHYSIV 567

| | | | |
|-----------------------|---|---|---|
| OY | 588 | SIVODMIKRSQGLNLFQTFKFLHVTIR | 616 |
| Dd | 568 | AVLHDMLRHTDCKLSFLGFKVLLHGVSSR | 596 |
| <hr/> | | | |
| RESULT | 10 | | |
| ID | 004290 | PRELIMINARY: | PRT: 601 AA. |
| AC | 004290; | | |
| DT | 01-JUL-1997 | (TREMBLrel. 04, Created) | |
| DT | 01-JUL-1997 | (TREMBLrel. 04, Last sequence update) | |
| DT | 01-JUN-2001 | (TREMBLrel. 17, last annotation update) | |
| DE | CDCK-RELATED PROTEIN KINASE. | | |
| GN | CRK. | | |
| OS | Arbidopsis thaliana (mouse-ear cress). | | |
| OC | Eunaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | |
| OC | eustoids II; Brassicales; Brassicaceae; Arabidopsids. | | |
| OX | NCBI_TaxID=3702; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Salchert K.D.; | | |
| RL | Submitted (NOV-1996) to the EMBL/Genbank/DDBJ databases. | | |
| CC | -I- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES. | | |
| CC | -I- SIMILARITY: TO EF-HAND FAMILY. | | |
| DR | EMBL: Y09418; CAA70572.1; -. | | |
| DR | HSSP; Q63450; IAO6. | | |
| DR | Mendel; J3807; Atrah.1112;13807. | | |
| DR | InterPro: IPR002048; EF-hand. | | |
| DR | InterPro: IPR000719; Euk.pkinase. | | |
| DR | InterPro: IPR002290; Ser_thr_kin_actsite. | | |
| DR | Pfam; PF00036; ethand; 1. | | |
| DR | Pfam; PF00069; pkinase; 1. | | |
| DR | SMART; SMO0220; S_TKC; 1. | | |
| DR | PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1. | | |
| DR | PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. | | |
| DR | PROSITE; PS00108; PROTEIN_KINASE_ST; 1. | | |
| KW | ATP-binding; Calcium-binding; Serine/threonine-protein kinase; | | |
| KW | Transferase. | | |
| SQ | SEQUENCE 601 AA; 67006 MW; 61B450317AC25DBF CRC64; | | |
| <hr/> | | | |
| Query Match | 58.6%; | Score 1911; | DB 10; Length 601; |
| Best Local Similarity | 60.3%; | Pred. No. 2.3e-126; | |
| Matches 379; | Conservative 87; | Mismatches 117; | Indels 46; Gaps |
| OY | 1 | MGQCCKGKSGAGTADDEGGVTEHOSPPANGLPST--- | PPROQAQAOAQOQGTPRRRG 56 |
| Dd | 1 | MCLCTSKPRSSNS----- | DOTPARNSPLPASSESVKPSSSSYNGEDCVTTTNNG 50 |
| OY | 57 | SKSG----- | STTPGHQTGPVAMPSPBPSCGASPLDAGVSPSPARSTPRFRFRPEPPSP 111 |
| Dd | 51 | KKSPPFPFYSPSPAHYFSKTKPARSPATNSP----- | NSPKRFKFRPEPPSP 99 |
| OY | 112 | AKHITATLAKRIGGGRKREGTIPEGCGVGAGCGGGCAGADGAETERPLDKTDFGSKNFGAK | 171 |
| Dd | 100 | AKHIAVALARRGVSVPKNSSAIPE--GSEAEGGGVG----- | LDSKFSGSKSFASK 147 |
| OY | 172 | YELGEVGGHGHHGCSAAYKKKGGOVAANKITIAKAMTAISTEDVRREVKITIRALS | 231 |
| Dd | 148 | YELGVEVGHGHHGYCAAEFKKGDDNKGOOVAKVIPKAMTTATAIEDVRREVKITIRALS | 207 |
| OY | 232 | GNNNLVVKFEFDACEDDLNVYIVMELEGGELDIRIIARGRYEEDAOKAIVOILSVAFG | 291 |
| Dd | 208 | GNNNLPHFFDAEDHDNDNYIVMELEGGELLDRILLISRGSKTYEBEADAKYMIQLLNVAFC | 267 |
| OY | 292 | HLOGVVHRDLKENFLFTTRDENAPMKLIDFGLSDFIPTDERLNDIVGSAYVAPEVLHR | 351 |
| Dd | 268 | HLOGVVHRDLKEPFENLETSEKEDTSOLKAIDFGLSDVPRDERLNDIVGSAYVAPEVLHR | 327 |
| OY | 352 | SYSMEADIWSIGVITYIILCGSRPMARRESGISFVSLADNFEDSPMPPTYSAEKADV | 411 |
| Dd | 328 | YSTSTADITSVGIYYIILCGSRPMARRESGISFRAVLKADSFDPPMLLSSEARDV | 387 |

| | | | |
|---|---|---|--------------|
| OY | 412 | KRFKDYRKMTVAOALHTTHMLNR-EGORJLDILIRLJKOYLRAAPRLKLAKLSK | 470 |
| | | : : : : : : : : : : : : : : | |
| Db | 388 | KRLNKDPRKKLTAAQALSHPWIKDSNDKAKPMDILVFKIMRAYIRSSLSKKAAIRLSK | 447 |
| OY | 471 | ALREDELLYLKLOFKLLEP-RDGFSVLDFNTFATLRVLTADAMKESRVLFLHALEPLAYR | 529 |
| | | : : : : : | |
| Db | 448 | TLYVDLFELYLEGOFALLBEPKNGTISLENIKSLMKMATDMKDRIPELGQSALQYR | 507 |
| OY | 530 | RMDPEEFCAALISPOLALERWELIAGTAQOPBOENRYISVELAQEINLAFT--HY | 587 |
| | | : : : : : : : : : : | |
| Db | 508 | RMDEEEFCFAALSYHQULDALDRMEDHACAAELEKEGNRPIMDELASGLGPSVPVH | 567 |
| OY | 588 | SIVODMIRSKDGLNLFGLTFKFLHCVTIR | 616 |
| | | : : : : : : : : : : : : : : : : : | |
| Db | 568 | AVLHDWLRLHTDOCKLSFLGFGVFKLOHCVSSR | 596 |
| RESULT | 11 | | |
| O9LET1 | | PRELIMINARY; | PRT; 577 AA. |
| AC | O9LET1 | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, Created) | | |
| DT | 01-Oct-2000 (TREMBLrel. 15, Last sequence update) | | |
| DT | 01-JUN-2001 (TREMBLrel. 17, Last annotation update) | | |
| DE | CALCIUM-DEPENDENT PROTEIN KINASE-LIKE. | | |
| GN | TBM16.90. | | |
| OS | Arabidopsis thaliana (Mouse-ear cress). | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | |
| OX | eurosidis II; Brassicales; Brassicaceae; Arabidopsids. | | |
| NCBI_TaxID=3702; | | | |
| N | [1] | | |
| NP | SEQUENCE FROM N.A. | | |
| RA | Benes V., Wumbach E., Drzonek H., Ansozge W., Mewes H.W., Rudd S., | | |
| RA | Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; | | |
| RL | Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases. | | |
| CC | -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES. | | |
| DR | EMBL; AL390921; CAC00739.1; -. | | |
| DR | InterPro; IPR000719; Euk_Pkinase. | | |
| DR | InterPro; IPR002290; Ser_thr_kin_actsite. | | |
| DR | Pfam; PF00069; Pkinase; 1. | | |
| DR | SMART; SM00230; S_tkc; 1. | | |
| DR | PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1. | | |
| DR | PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. | | |
| DR | PROSITE; PS00108; PROTEIN_KINASE_ST; 1. | | |
| KW | ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase. | | |
| SO | SEQUENCE 577 AA; 64547 MW; 7E1EA8A8E48BC934 CRC64; | | |
| Query Match | 56.1%; Score 1829; DB 10; Length 577; | | |
| Best Local Similarity | 56.7%; Pred. No. 1.3e-120; | | |
| Matches 355; Conservative 100; Mismatches 107; Indels 64; Gaps 7; | | | |
| OY | 1 | MGC0GKAASGTADDDEGGVYTHEHSPPPANCLPTSTPPNQQAQAQQVGTFRRRGSKSG | 60 |
| | | : : : : | |
| Db | 1 | MGLCHGR-----PIEQSNLPISNEIEETPKNSSOKAS----- | 35 |
| OY | 61 | STTPHGQRGVAMPSPYPGSGASPDA-----GVSPPARSTPRFPKPPPPSPPAKH | 114 |
| | | : : : : | |
| Db | 36 | --SGFFPYSPPLPSLEKTSPAVVSSSVSTPLRIKRPPPPSPPAKH | 81 |
| OY | 115 | IKATLAKRLGGGPKPECTIPREGGVAGAGGGGAADGAEFTERPLDKTGFSKNFGAKYEL | 174 |
| | | : : : : : : : : | |
| Db | 82 | IRALLARRHGSVKPNEASIPE-----GSCPCEGLDKKCFGSQFASHYEI | 126 |
| OY | 175 | GKEVGRRGFHGTCSAVVKKGEKGCTVAVKIATAKMMTTAISIEDVRRPVKTLRALSGIN | 234 |
| | | : : : : : : : : | |
| Db | 127 | DGEVGRGHFGYTCSKGGKSLGDGVAVKVYLPKSKMTTALAIDEVRRRVKTLLRALTGHK | 186 |

DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR002719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TYKc; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; Transferase.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 606 AA; 67972 MW; 535329AD5F89B14C CRC64;

Query Match 54.0%; Score 1760.5; DB 10; Length 606;
 Best Local Similarity 59.7%; Pred. No. 9.1e-116;
 Matches 357; Conservative 74; Mismatches 104; Indels 63; Gaps 11;

QY 64 PGHQTGVAMPSPYPSGG-ASPLPAGVSPSPAR-----STPRPFK 103
 DB 32 PDKS-PIPTPSAKASPPFPYTPSPAHRRNKSNDVGGGSGSKLTSTPLQLR 88
 QY 104 RPPPPSPAKHIKATLAKRLGSGKPKEGT-----PEEGVGAGGGGGAD 150
 DB 89 RAHPSPAKHIAALRRRG---KKFALSGVTQLTTEVPQREBEVGE----- 135
 QY 151 GAETERRLDKTFGFSKNFGAKYELGKEVGRGHRGHTCSAAVVKGEYKQGVAAKIIAKAK 210
 DB 136 -----LDRKFGFSKFEHRSVELGEIGRGHGYTCSAKFKKGLKGQYAAVKIIIPKSK 188
 QY 211 MTTAISIEDVRREVKKILRALSGHNNLVKFPDAGEDGLNVYIMELCGSGELDRILARGG 270
 DB 189 MTTAISIEDVRREVKKILRALSGHNNLVKFPDAGEDGLNVYIMELCGSGELDRILARGG 248
 QY 271 RYTEDAKAIIVQILSVAFCHGQVVRDLKPENFLFTTREDENAPMKLIDFGISDFIRP 330
 DB 249 KYSENAKAPVITQILNVVACHGQVVRDLKPENFLFTTREDENAPMKLIDFGISDFIRP 308
 QY 331 DEFLNDIVGSAYVAPEVLRHRSYMEADWSIGVITYILLGSRPFMARTESGIFRSVLR 390
 DB 309 DEFLNDIVGSAYVAPEVLRHRSYMEADWSIGVITYILLGSRPFMARTESGIFRSVLR 368
 QY 391 ADNFDDSPWPTVSAEADDFKRLNDRKRYKMTAVOALTHPMLR--DEGROIPLDLIR 448
 DB 369 ADNFDDSPWPTVSAEADDFKRLNDRKRYKMTAVOALTHPMLR--DEGROIPLDLIR 428
 QY 449 RLKQYLRATPLKRLAKLSKALREDELLYLKQFLKEP-RDGEVSLDNFRTALRYL 507
 DB 429 ROKKAVLRSSSLKRALRALSKLTLKDELLYLKQFLSLAPNKGDLITMTIRALASNA 488
 QY 508 TDMKESRVLEFLHLEPLAYRRMDPEEFCAAIISPYQLEALERMEIAGTAQOEQEG 567
 DB 489 TEAMKESRVLEFLHLEPLAYRRMDPEEFCAAIISPYQLEALERMEIAGTAQOEQEG 548
 QY 568 NRVISVEELAQELNLAFT--HYSIVODMIRKSDGKLNFLGFTFKLHGVTIR--GSNTR 621
 DB 549 NRVISVEELAQELNLAFT--HYSIVODMIRKSDGKLNFLGFTFKLHGVTIR--GSNTR 606

RESULT 14
 081088 PRELIMINARY; PRT; 415 AA.

AC 081088;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CDPK-RELATED PROTEIN KINASE (FRAGMENT).
 GN CRK1
 OS Tradescantia virginiana (Virginia spiderwort).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinales; Commelinaceae;
 OC Tradescantia.
 OX NCBI_TaxID=59016;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-STAMEN HAIR;
 RA Sukanya R., Molniak S.M.;
 RT "A CRK like sequence from Tradescantia virginiana."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AF009337; AAC24961.1; -.
 DR HSSP; P00523; 2PTR.
 DR Mendel; 31742; Travl; 1112; 31742.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR002719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00036; efhand; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Calcium-binding; Serine/threonine-protein kinase;
 KW Transferase.
 FT NON_TER
 SQ SEQUENCE 415 AA; 47875 MW; 623EF3DE54EDB21 CRC64;

Query Match 53.7%; Score 1749.5; DB 10; Length 415;
 Best Local Similarity 81.5%; Pred. No. 3.1e-115;
 Matches 339; Conservative 37; Mismatches 35; Indels 5; Gaps 3;

QY 212 TTTAISIEDVRREVKKILRALSGHNNLVKFPDAGEDGLNVYIMELCGSGELDRILARGG 271
 DB 1 TTTAISIEDVRREVKKILRALSGHNNLVKFPDAGEDGLNVYIMELCGSGELDRILARGG 60
 QY 272 YTEDAKAIIVQILSVAFCHGQVVRDLKPENFLFTTREDENAPMKLIDFGISDFIRP 331
 DB 61 YTEDAKAIIVQILSVAFCHGQVVRDLKPENFLFTTREDENAPMKLIDFGISDFIRP 120
 QY 332 ERLNDIVGSAYVAPEVLRHRSYMEADWSIGVITYILLGSRPFMARTESGIFRSVLR 391
 DB 121 ERLNDIVGSAYVAPEVLRHRSYMEADWSIGVITYILLGSRPFMARTESGIFRSVLR 180
 QY 392 DPNFDDSPWPTVSAEADDFKRLNDRKRYKMTAVOALTHPMLR--DEGROIPLDLIR 451
 DB 181 DPNFDDSPWPTVSAEADDFKRLNDRKRYKMTAVOALTHPMLR--DEGROIPLDLIR 240
 QY 452 KOYLRAATPLKRLAKLSKALREDELLYLKQFLKEP-RDGEVSLDNFRTALRYL 510
 DB 241 KVLRAATPLKRLAKLSKALREDELLYLKQFLKEP-RDGEVSLDNFRTALRYL 300
 QY 511 MKESRVLEFLHLEPLAYRRMDPEEFCAAIISPYQLEALERMEIAGTAQOEQEG 570
 DB 301 MKESRVLEFLHLEPLAYRRMDPEEFCAAIISPYQLEALERMEIAGTAQOEQEG 360
 QY 571 ISVEELAQELNLAFT--HYSIVODMIRKSDGKLNFLGFTFKLHGVTIR--GSNTR 623
 DB 361 ISVEELAQELNLAFT--HYSIVODMIRKSDGKLNFLGFTFKLHGVTIR--GSNTR 415

RESULT 15
 09XGW6 PRELIMINARY; PRT; 594 AA.

AC 09XGW6;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CDPK-RELATED KINASE 2 (FRAGMENT).
 GN CRK2
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CV, COLUMBIA; TISSUE-SEEDLING HYPOCOTYL;
 RA Choi J.H., Lala H.;
 RT "CDPK-related kinases in Arabidopsis";
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 CC -! SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF153352; AAD38059.1; -.
 DR HSSP: O63450; 1A06.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 SEQUENCE 594 AA; 66757 MW; C21D97BCAD2440B CRC64;

Query Match 53.3%; Score 1736.5; DR 10; Length 594;
 Best Local Similarity 59.9%; Pred. No. 4.3e-114;
 Matches 355; Conservative 75; Mismatches 120; Indels 43; Gaps 9;

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 QY 96 --STPRREFKRPFPSPAKHIKATLAKRLGGKPKKEGTIPDEGCVAGGGGGADGAE 153
 DB 72 VTSTPLQLQALAFHPSPARHIDVLR--KERKEALP-----AARQKEE 117
 QY 154 TERP--LDKTFGSKNFGAKYELGKEVGGRGHFGHTCSAVVKKGEYKQTVAAVITAKK 210
 DB 118 EEREVEGLDKRFGSKELSGRIELGEGIRGHFGYTCSAKFKGELDQEVAAVITPKSK 177
 QY 211 MTTAISTEDVAREVKILRALSGHNNLVKFTDACEDGLNVIYIMELCEGELLRIARGG 270
 DB 178 MTSAISIEDVAREVKILRALSGHNNLVKFTDACEDGLNVIYIMELCEGELLRIARGG 237
 QY 271 RYTEEDAKAIYVOILSVVAFCHLOGVVHRLKPNELFTTRDENAPMKLIDFGISDFIRP 330
 DB 238 KYSDDDAKAVLIQILNVVAFCHLOGVVHRLKPNELFTSKENSMKLVIDFGISDFVRP 297
 QY 331 DERLNDIVGSAYVYAPVFLHRSYSMEADIVSIGVITYILLGSRPFWARTESGIFRSVLK 390
 DB 298 DERLNDIVGSAYVYAPVFLHRSYSMEADIVSIGVITYILLGSRPFWARTESGIFRSVLK 357
 QY 391 ADPNFDDSPWPTVSAEKADVVKRFLNKDYRKMTAVOALTHPWLDEOR-QIPDLILIFR 449
 DB 358 ADPSFDEPPWPSLSFEKADVVKRFLNKDYRKMTAVOALTHPWLDEOR-QIPDLILIFR 417
 QY 450 LIKQVLAATPLKRLAKLSKALREDELTYLKIOLFLLRP-RDGFVSLDNFRALTIRYL 508
 DB 418 QIKAYLRSSSLRKRAALMALSKITLTDELTYLKIOLFLLRP-RDGFVSLDNFRALTIRYL 477
 QY 509 DANKESRVLEFLHALRPLAYRRMDFEEFCNAATSPYOLEALRMEETIAGAFQFOEGN 568
 DB 478 EAMKESRIPDFLLALNGIDQYKMDFEFCASISVGHESLDCWEOGSIHAYELFEMNGN 537
 QY 569 RVISVEELAOELNA--PTHYSIVODWIRKSDGKLNFLGFTKFLHGVTIRGS 618
 DB 538 RVIVIEELASLGVSISIPVH-TILNDWIRHTDGKLSFLGFTVXLLHGVSIRGS 589

Search completed: May 2, 2002, 08:47:59
 Job time: 628 sec

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| Dd | 655 | tgtagagccgccctcaattgcttcaattgctatggaattatgtaaggctggaagtgtgcta | 714 |
| OY | 981 | gacgaataattagccagagggccgggagatacacagaggaagatgccaagcgattctgtca | 1040 |
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| Dd | 835 | CCAGAGAAATTTTCCTTCACACAGAGAGTAAGGAGGCTCCATATGATGATTGATCTTT | 894 |
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| OY | 1281 | gggtctcaaaagctacatctctgctctgttgagcgtcgccatctcgggacagaaacatca | 1340 |
| Dd | 1015 | GGTGTATTAACATCATCTTGTCTGTCTGGCAGTGGCCATCTCGGGACAGACAGATCT | 1074 |
| OY | 1341 | ggaaattatccgaatcgttggttgtagagctgatacccaactttgatagtattcaacgtgactaca | 1400 |
| Dd | 1075 | GGGATCTTCGGGTCCGATTTAGAGGGCTGATCCCAATTTTGAAGATTCACATAGGCTTCA | 1134 |
| OY | 1401 | gtatccagctgtagagctaaagatacttctgtgaagagatacttctgaacaaagatataccgcaaa | 1460 |
| Dd | 1135 | GTATCGGCTGAGGCTTAGAGATTTTGTGAAGAGATTTCTGAACAAAGATTAACCGCAAAAGA | 1194 |
| OY | 1461 | atgagccgtgttgaagacgtactatcccttggttgtagagatagaaacaaaggagaatcccg | 1520 |
| Dd | 1195 | ATGATGTGTGCCAGAGACTGACTACCCCTGGTTTACGAGATGAACAAAGGCAAAATTTCCA | 1254 |
| OY | 1521 | cttggaacatactcatctcagatattaatlaagcaaaatacctccgcgtacacctctctaaacgg | 1580 |
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| OY | 1581 | tttgcatattaaagagcactataccaagagctttaaagggaagatgaaacttttgatctcaaatg | 1640 |
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| Dd | 1435 | CTGCAAGATACTCAACTGACGCCCATGAGAGATCAAGGGTCTTGAGTTTCAGATTCGC | 1494 |
| OY | 1761 | tttgaaacacacttgatactaaagaagaatggactttgaaagatttgctgcgcacgaatttcagc | 1820 |
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| OY | 1821 | ccttacacagcttgtaggcacctggaagaaggtggaggaagatttgcctggaacagctcttccaaga | 1880 |
| Dd | 1555 | CCGTACACAGCTGGAAAGCTTTGGAAGGTGGGAAGAAATTGCTGGAAACAGCTTTTCAGCAC | 1614 |
| OY | 1881 | tttgaacaagaagggaacagagtcataatacagtttgaggaattagcacaggaattaaactt | 1940 |
| Dd | 1615 | TTTGCAAAAGAGGGCAACCGAGTTTATATAGTTTGAAGATTTGACACAGAACTAAATCTC | 1674 |
| OY | 1941 | gtccaacatattacccaactgcttcaagagctgatacaagaataaccgatgggcaagctaaac | 2000 |
| Dd | 1675 | GGCGCGACACATTATCTCATTTGTGCAAAGACTGTGATCCAGAAATTCGAGAGCGCAACTTATAC | 1734 |
| OY | 2001 | tttctcgggttaccaaatttttacaatggttgctacaataaaggaggtctcaatatacaagag | 2060 |

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| Db | 1735 | TTTTCTGGGTTACCAAAATTTTGCACGGGTGCACGATACGGGGTTCAATATACAAACACA | 1794 |
| Oy | 2061 | catlaagcagatttgcacaaagaatgtaattcttcttccttaatttlaagccgcatac | 2120 |
| Db | 1795 | CACCTAAGCAGATGACAAACTGATGTGGCTTTTAAATTGGAGCCCTC-----CATCGAT | 1846 |
| Oy | 2121 | tatgtagccctgatttgatgttttccccc-----cctgcctccatccctctgltcaataag | 2175 |
| Db | 1847 | TATATGGCCCTCATTTGCTGTGTACCTACCTCCGCGCCCTGCCCTGCCCTCGAGCTGTGTCA | 1906 |
| Oy | 2176 | atccattatcttgcctgcgtgcgtgcgtgttgcacatcaagtttttctagaagaata | 2235 |
| Db | 1907 | ATGACCAATCCTGTTTGTGTATGCC-CCCTCCGCGCTGTGGCCGTCTTTTGTATAGATA | 1965 |
| Oy | 2236 | catglaaagatcttttctglaag--aatcgaatgabatgtttgttcaagaatatagat | 2292 |
| Db | 1966 | CATGTAAGAATCCTGTATATGCGCAAAATCATATGTTTGTCTCAAGAAATATATAGTGTCA | 2025 |
| Oy | 2293 | catgttgttcttttttgcacgaata | 2317 |
| Db | 2026 | TTTTGTTCTTTTTTTGGCTCGCTAA | 2050 |

| RESULT | 3 | | | |
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| LOCUS | MZECDEPKB | 2228 bp | mRNA | PLN |
| DEFINITION | Zea mays mRNA for CDPK-related protein kinase, complete cds, clone zmcCRK3. | | | |
| ACCESSION | D84508 | GI:1313908 | | |
| KEYWORDS | CDPK-related protein kinase; calcium-dependent protein kinase-related kinase; CRK. | | | |
| SOURCE | Zea mays (strain:Inbred line H84) Root cDNA to mRNA, clone_1lb:lambda gt10 clone:zmcCRK3. | | | |
| ORGANISM | Zea mays | | | |
| REFERENCE | Eukaryotes: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; PAC clade; Panicoideae; Andropogoneae; Zea. | | | |
| AUTHORS | 1 (bases 1 to 2228) | | | |
| TITLE | Furumoto,T., Ogawa,N., Hata,S. and Izui,K. | | | |
| JOURNAL | Direct Submission | | | |
| | Submitted (27-APR-1996) to the DDBJ/EMBL/Genbank databases. | | | |
| | Tsuyoshi Furumoto, Kyoto University, Graduate School of Agriculture Lab. of Plant Physiology, Sakyo-ku, Kyoto, Kyoto 606-01, Japan (E-mail:tsuyo@kais.kyoto-u.ac.jp, Tel:075-753-6142, Fax:075-753-6146) | | | |
| REFERENCE | 2 (sites) | | | |
| AUTHORS | Furumoto,T., Ogawa,N., Hata,S. and Izui,K. | | | |
| TITLE | Plant calcium-dependent protein kinase-related kinases (CRKs) do not require calcium for their activities | | | |
| JOURNAL | FEBS Lett. 396 (2-3), 147-151 (1996) | | | |
| MEDLINE | 97072168 | | | |
| FEATURES | Source | | | |
| | Location/Qualifiers | | | |
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RESULT 4
D38452 1784 bp mRNA PLN 27-SEP-1997
LOCUS D38452
DEFINITION Zea mays mRNA for calcium-dependent protein kinase-related kinase,
partial cds.
ACCESSION D38452
VERSION D38452.1 GI:2443387
KEYWORDS calcium-dependent protein kinase-related kinase.
SOURCE Zea mays (strain:Inbred line H84, haplotype:2) Seedling Leaf cDNA
to mRNA, clone_11b:lambda gt10 clone:ZMPK650.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1784)
AUTHORS Izui, K.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1994) to the DDBJ/EMBL/Genbank databases. Katsura
Izui, Kyoto University, Agricultural Biology; Oiwake-cho,
Kitsashirakawa, Sakyo-Ku, Kyoto 606-01, Japan
(Tel:075-753-6140, Fax:075-753-6146)
2 (sites)
Furumoto, T., Ogawa, N., Hata, S. and Izui, K.
REFERENCE Plant calcium-dependent protein kinase-related kinases (CRKs) do
not require calcium for their activities
JOURNAL FEBS Lett. 396 (2-3), 147-151 (1996)
MEDLINE 97072168
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Best Local Similarity 83.5%; Pred. No. 2.3e-161;
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QY 768 aagaaggaggagatcacagagacagccgtcgcgctcaagatcatcgccaaagctaaagtg
DB 61 AAGAAAGGCGACACAAAGGCCATACCGTCGCCGCTCAAGATCATCTCCAAGACTAAGTG 120
QY 828 acaacggcaatcatcatgaggaatgctgtagagaaagtaaaattttgaggcgtatca 887
DB 121 ACAAGGGCATTTCCATTCAGAGATTGCTGTAGGGAGGTCAGAGATTTTAAAGCCCTTTCA 180
QY 888 gggcacaataatctcgtaaatctatgtaagatgtagagtaggctcaatgctacatt 947

DB 181 GGGCAGCATTAATCTCGACATCTCATGATCATGTGAGACGCCCTCAATGCTACATT 240
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QY 2317 a 2317
Db 1609 A 1609

RESULT 5
AF009337
LOCUS AF009337 1562 bp mRNA PLN 01-JUL-1998
DEFINITION Tradescantia virginiana CDPK-related protein kinase (CRK1) mRNA,
AF009337
ACCESSION AF009337
VERSION AF009337.1 GI:3282249
KEYWORDS
SOURCE Virginia spiderwort.
ORGANISM Tradescantia virginiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Commelinales;
Commelinaceae; Tradescantia.
1 (bases 1 to 1562)
Sukanya, R. and Molniak, S.M.
A CRK like sequence from Tradescantia virginiana
Unpublished
2 (bases 1 to 1562)
Sukanya, R. and Molniak, S.M.
Direct Submission
Submitted (18-JUN-1997) Plant Biology, University of Maryland, H.J.
Patterson Hall, College Park, MD 20742, USA
JOURNAL
TITLE
AUTHORS
REFERENCE
REVIEWED
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BASE COUNT 474 a 287 c 336 g 465 t
ORIGIN

Query Match 31.0%; Score 736.2; DB 8; Length 1562;
Best local Similarity 76.5%; Pred. No. 1.2e-101;
Matches 916; Conservative 0; Mismatches 278; Indels 3; Gaps 1;

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QY 1126 gggatgaaatgtcccatgaagtgtgatttggctctcctgattcattagaccag 1185
Db 301 GAGATGGAATGCTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
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Db 361 ATGAAGACATAAATGATATGTTGGAAGCCCATATCTATGTGGCACCAGATCCTGTGAC 420
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Db 421 GATCATACATATGAGGAGCGACATATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG 480
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QY 1366 ctgactccaacttgatgattcaccgctgacctacagatcaagctgaagcttaagatttg 1425
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Db 841 ATGATGCGGCTGATCTCCCTTGAATAATTTCCACACAGACTAGGCCAATAATGCTACTAAG 900
QY 1723 ctatgaagaatcagaggttcttgaattttagcatgctgtggaaccaactgtcatacagaa 1782
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 Oy 1985 cgaatgcaagctaaactttctcgtgttaccaaatcttaccatggtgt 2032
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RESULT 8
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 DEFINITION Arabidopsis thaliana CDPK-related kinase 2 (CRK2) mRNA, partial
 ACCESSION AF153352
 VERSION AF153352.1 GI:5020367
 KEYWORDS thale cress.
 SOURCE Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
 1 (bases 1 to 2005)
 AUTHORS
 Chol, J.H. and Lala, H.
 CDPK-related kinases in Arabidopsis
 unpublished
 2 (bases 1 to 2005)
 Chol, J.H. and Lala, H.
 Direct Submission
 Submitted (21-MAY-1999) School of Biology, Georgia Institute of
 Technology, MC 0230, Atlanta, GA 30332-0230, USA

FEATURES
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BASE COUNT 582 a 409 c 494 g 520 t
 ORIGIN

Query Match 26.1%; Score 618.8; DB 8; Length 2005;
 Best Local Similarity 65.4%; Pred. No. 5,2e-84;
 Matches 973; Conservative 0; Mismatches 502; Indels 13; Gaps 4;

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 Oy 659 gagggcattggaagaagcgttcggtgttcgaagaacttcggtcggaagctcgg 718
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 Oy 719 gaagaggtgtggtgagggcacttcggaacacactgtcctccgcgcgtcaaaagggcga 778
 Db 426 GGAAGAGATTGGGAGAGGCAATTTTGGGTATCTTGCTCTGCTTAAGTTCAAGAAAGAGA 485
 Oy 779 gtacaaaggaagacgctgcgcgtcaagaatcgcgaagaagatgaagaagcgaat 838
 Db 486 GCTCAAGATCAGAGAGGTTGCTGTTAAAGTATCCCAAAATTAAGATGACATCGCAT 545
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 Db 546 ATCTATTAGAGATGTGAAGAAGAAATTAAGTCTGGGCGGTATCTGGACATCAAAA 605
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 Db 1926 TGCACATGCTGTCTCTA 1943
 RESULT 11
 AF153351
 LOCUS
 DEFINITION
 Arabidopsis thaliana CDPK-related kinase 1 (CRK1) mRNA, complete cds.
 ACCESSION
 AF153351
 VERSION
 AF153351.1
 KEYWORDS
 SOURCE
 ORGANISM
 thale cress.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE
 1 (bases 1 to 2148)
 AUTHOR
 Choi, J.H. and Lala, H.
 TITLE
 CDPK-related kinases in Arabidopsis
 JOURNAL
 2 (bases 1 to 2148)
 REFERENCE
 Choi, J.H. and Lala, H.
 AUTHORS
 Direct Submission
 TITLE
 Submitted (21-MAY-1999) School of Biology, Georgia Institute of Technology, MC 0230, Atlanta, GA 30332-0230, USA
 JOURNAL
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 BASE COUNT 585 a 411 c 493 g 659 t

ORIGIN

Query Match 24.2%; Score 574.8; DB 8; Length 2148;
 Best Local Similarity 63.5%; Pred. No. 2,1e-77;
 Matches 930; Conservative 0; Mismatches 522; Indels 12; Gaps 3;

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 QY 2068 cgaattgcaaaagaagaatgattc 2091
 DB 1844 CCATTGTTAATGATGAAGAGATGC 1867

RESULT 12
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 DEFINITION
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 complete cds.
 AF194413
 VERSION
 AF194413.1 GI:6689919
 KEYWORDS
 SOURCE
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 Oryza sativa.
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoae; Oryza.
 1 (bases 1 to 1917)
 Cheong, Y.H., Moon, B.C. and Cho, M.J.
 Isolation of calcium-dependent protein kinases from rice
 Unpublished
 2 (bases 1 to 1917)
 Cheong, Y.H., Moon, B.C. and Cho, M.J.
 Direct Submission
 Submitted (13-OCT-1999) Biotechnology, Gyeongsang National
 University, Gwaja dong, Chinju, Kyungnam 660-701, Korea
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ACCESSION AF194414
VERSION AF194414.2 GI:12592068
KEYWORDS
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
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AUTHORS Cheong Y.H., Moon,B.C. and Cho,M.J.
TITLE Isolation of calcium-dependent protein kinases from rice
JOURNAL unpublished
REFERENCE 2 (bases 1 to 1828)
AUTHORS Cheong,Y.H., Moon,B.C. and Cho,M.J.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1999) Biochemistry, Gyeongsang National
University, Gwaza dong, Chinju, Kyungnam 660-701, Korea
REFERENCE 3 (bases 1 to 1828)
AUTHORS Cheong,Y.H., Moon,B.C. and Cho,M.J.
TITLE Direct Submission
JOURNAL Submitted (29-JAN-2001) Biochemistry, Gyeongsang National
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REMARK Sequence update by submitter
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ACCESSION
AF289237
VERSION
AF289237.1 GI:9858872
KEYWORDS
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ORGANISM
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
1 (bases 1 to 7359)
Lu,Y.-T., Liang,S. and Wang,L.
Cloning of a calcium/calmodulin-dependent protein kinase gene, MCK2
from maize
Unpublished
2 (bases 1 to 7359)
Lu,Y.-T., Liang,S. and Wang,L.
Direct Submission
Submitted (25-Jun-2000) Center for Developmental Biology, College
of Life Sciences, Wuhan University, Wuhan, Wuhan, Hubei 430072,
China

FEATURES
source

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RESULT 15
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Sequence 18 from Patent WO0107592.
ACCESSION
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VERSION
AX077711.1 GI:13122086
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potato.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanales; Solanales; Solanum.
REFERENCE
1 (bases 1 to 2210)
Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.
Herbicide resistant plants and methods for the production thereof
Patent: WO 0107592-A 18 01-FEB-2001;
JOURNAL
ZENECA LIMITED (GB)
FEATURES
Location/Qualifiers
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Best Local Similarity 56.1%; Pred. No. 1.5e-33;
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GenCore version 4.5
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| 3 | 533 | 22.5 | 1309 | 21 AAC49388 | Arabidopsis thaliana |
| 4 | 337.2 | 14.2 | 1781 | 21 AAC34898 | Arabidopsis thaliana |
| 5 | 283.4 | 11.9 | 2210 | 22 AAF74279 | Potato calcium dep |
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| 23 | 208.2 | 8.8 | 1506 | 21 AAC44687 | Arabidopsis thaliana |
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| 25 | 206.4 | 8.7 | 2022 | 22 AAF74285 | Vigna radiata calc |
| 26 | 205.6 | 8.7 | 1768 | 22 AAF74274 | Soybean calcium de |
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| 33 | 153 | 6.4 | 1400 | 16 AAC090495 | E. maxima Em70-1 a |
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| 36 | 128.4 | 5.4 | 582 | 21 AAC50455 | Arabidopsis thaliana |
| 37 | 127.8 | 5.4 | 1575 | 21 AAA70239 | Plasmodium falcipa |
| 38 | 126.8 | 5.3 | 1412 | 21 AAC51681 | zea mays DNA fragm |
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DT 17-Oct-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 68642.
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
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PD 06-SEP-2000.
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| PR | 15-SEP-1999; | 99US-0154018. |
| PR | 16-SEP-1999; | 99US-0154039. |
| PR | 20-SEP-1999; | 99US-0154779. |
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| PR | 23-SEP-1999; | 99US-0155486. |
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PR 17-AUG-1999; 99US-0149175.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 14.28; Score 337.2; DB 21; Length 1781;
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DB 1589 ag 1590

RESULT 5

AAE74279 standard; DNA; 2210 BP.

AAE74279;

04-MAY-2001 (first entry)

Potato calcium dependent protein kinase clone.

Calcium dependent protein kinase; CDPK; herbicide resistance;

Paranquat; diquat; crop production; ds.

Solanum tuberosum.

WO200107592-A2.

01-FEB-2001.

26-JUL-2000; 2000MO-GB02876.

27-JUL-1999; 99GB-0017642.

(ZENE) ZENECA LTD.

Holt CD, White AJ, Michael AJ, Osborn RW;

WPI; 2001-168549/17.

Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole

Claim 18; Page 40-41; 50pp; English.

The present invention describes a method of producing plants which are resistant to the herbicides paranquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

Sequence 2210 BP; 682 A; 382 C; 510 G; 636 T; 0 other;

Query Match 11.9%; Score 283.4; DB 22; Length 2210;
Best Local Similarity 56.1%; Pred. No. 1.4e-48;
Matches 646; Conservative 0; Mismatches 481; Indels 24; Gaps 5;

QY 786 gacagacccgtccgcctcaagatcagtcgcaagactaagatgacaaagggacatccatc 845
DB 493 ggaagctctgtggcgtgtcaaaaagaattgaaaaaacaagatggtctctccatgtcggt 552
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DB 553 gaggatctgaagaagcgaagatcaagatatgaagccttagtctcaltgaaatggtgtc 612
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DB 613 caattctataatctatctgaaagataatattatgtctacatcgttaactgtgattgtgaa 672
QY 966 ggaaggaattgtctagaacagataltagccagagcggtgagatatcacagaggaatgcc 1025
DB 673 ggtgagaactattggcagatgtgcaaaagaacgtcg-----tatacgaagaatgca 726
QY 1026 aaagcagatgtgtgacagaatttgaagcgttagtgccttctcatcttcagggttagtg 1085
DB 727 gcaatagctgtaaccagatgtctaaagtgtagcgtgagcttattacatgtgttggtg 786
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DB 787 catcgtatatagaacactggaatttctctctcaagtcaagaagagatcttaccatca 846
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| PR | 11-AUG-1999; | 99US-0148319; |
| PR | 12-AUG-1999; | 99US-0148341; |
| PR | 13-AUG-1999; | 99US-0148565; |
| PR | 13-AUG-1999; | 99US-0148684; |
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| PR | 04-OCT-1999; | 99US-0157117; |
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| PR | 13-OCT-1999; | 99US-0159294; |
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| PR | 14-OCT-1999; | 99US-0159638; |
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| PR | 21-OCT-1999; | 99US-0160767; |
| PR | 21-OCT-1999; | 99US-0160768; |
| PR | 21-OCT-1999; | 99US-0160770; |
| PR | 21-OCT-1999; | 99US-0160814; |
| PR | 21-OCT-1999; | 99US-0160815; |
| PR | 22-OCT-1999; | 99US-0160980; |
| PR | 22-OCT-1999; | 99US-0160981; |
| PR | 22-OCT-1999; | 99US-0160989; |
| PR | 25-OCT-1999; | 99US-0161404; |
| PR | 25-OCT-1999; | 99US-0161405; |
| PR | 25-OCT-1999; | 99US-0161406; |
| PR | 26-OCT-1999; | 99US-0161359; |
| PR | 26-OCT-1999; | 99US-0161360; |
| PR | 26-OCT-1999; | 99US-0161361; |
| PR | 28-OCT-1999; | 99US-0161970; |
| PR | 28-OCT-1999; | 99US-0161982; |
| PR | 28-OCT-1999; | 99US-0161993; |
| PR | 28-OCT-1999; | 99US-0162142; |

| | Query Match | 10.88: | Score 255.8: | DB 21: | Length 1677: | |
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| | Best Local Similarity | 52.08: | Pred. NO. 5.7e-43: | | | |
| | Matches 635: | Conservative 0: | Mismatches 547: | Indels 21: | Gaps | |
| Oy | 797 | cgcgcgtcaagatc | atgcgcgaagc | taagatgacacg | gcgcacatccatccattgagatgctcg | 856 |
| | | | | | | |
| | 369 | cgccttgatgaacat | atccacgaaggaag | tcttgatcttc | caagaagatcttaagagatctgac | 428 |
| Ob | | | | | | |

| | | | |
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| QY | 857 | ttgagaagcaaaaattttgaagcggttacagagcgcaaatatctccgtcaaatcttatga | 916 |
| DB | 429 | aagggagatcctcagataatgcatcatcttaagctcgtccacggtaagctacgtgacattaaagg | 488 |
| QY | 917 | tgcattctggagatgagcccaacatgctcacatctgcctagatattatgttgagggagaaatt | 976 |
| DB | 489 | agcttaacgagactctcttgatgtccactctgttaagagctcttgctcggagggagaaatt | 548 |
| QY | 977 | gctagacgaataattagccagagcgggagatcacagaggaagaattgccaaagcattgtc | 1036 |
| DB | 549 | gtttgataagatcatatcacaga---ggaattatatgtagaggaagatcgtcagctgac | 605 |
| QY | 1037 | tgtacaagatttgagagtgatgagctctctgtcatctccaggggtgaagtcgtgatt | 1096 |
| DB | 606 | taagatcatcttcggtgtgtgtggaagcgtgtcatctcgtgtgtgtgacgaagaagactc | 665 |
| QY | 1097 | gaagccagagaattctcctctttcacacccagggatgaaatgctccacatgaagtctatcga | 1156 |
| DB | 666 | gaagccgtagaattctcttatctgtttaataagaatgatctctctccacagactatcga | 725 |
| QY | 1157 | ttttgctcctctgattctcatatgaagccagatgaaagcgcttaatgtattgtttggaagtc | 1216 |
| DB | 726 | ctcttgagccatccgtccctcttcacacccagtcataatcatcatcgtatctgttggaagtc | 785 |
| QY | 1217 | atattatgttgcgccagaggtttctcacagatcatcatgtaatggaagacagacatttgag | 1276 |
| DB | 786 | ataatagtgtcctcgtgaggttttgtccaaagttatgagcgtggaagctgtatgttgagac | 845 |
| QY | 1277 | tattaggtgcataaagttacatctcgtctctgtgtagcagtcggccattctcgtgcacgaaga | 1336 |
| DB | 846 | tgcctgtgtatattgtataataatgtcttaagcggaaatccacactctcttgagacaaaca | 905 |
| QY | 1337 | atccagaaatctccagctcgtctgttagagcgtatcccaacttgaatgataccagtgagcc | 1396 |
| DB | 906 | gcgaaggatatttgatcgtcgtgtgtgaaagagataatcgactttgagtcagaccgtgagcc | 965 |
| QY | 1397 | tacagtatcacgtcgaagcgaatttctgtgaagaagattcttgaaacaaagaattacccgcaa | 1456 |
| DB | 966 | tgtgatatccgcacagtgctaaagaagattgataccgcgaagaatgtatctccaaagctgcaga | 1025 |
| QY | 1457 | aagaaatgacccgtgtctcaagcactgacatccactcgtgttgagaga-----tgaaacaaag | 1510 |
| DB | 1026 | acgcttgacccgtcatgaaagctctcgtgcatacccaatgagctcgtgagaaatgtgtgtgcc | 1085 |
| QY | 1511 | gcagatctcccgctgtagcatatcatctttcagaatlaattaaagcaataacctccgcgtacacc | 1570 |
| DB | 1086 | agatatagagcactatgaccagctgtctcttctccgtctcaagcaatctctgacatgaataa | 1145 |
| QY | 1571 | tccttaacggtgtgacattaaaggcactatcccaagcgtttaagggaagaatgaaactttgtta | 1630 |
| DB | 1146 | actaaagaagaatgagctttgaaaggttatatgactgtgagagtcctccgaaagagaagatacgtg | 1205 |
| QY | 1631 | tctcaaacgtcagctttaaactcgtctgaaacccagaaagatgtgtcttatcaactgtgacaact | 1690 |
| DB | 1206 | tttaagagagaatgtttcaagcaatgatacgtatbaaacgcggggcaatcatcaattgtatga | 1265 |
| QY | 1691 | tcgagcgcactaaacgcatacttaactgatagtatgaagaatcgaagggttcttgaatt | 1750 |
| DB | 1266 | actcaaaagctggtcgtgagaaaaatatyatacttataccttgaaagacacagatcatgatct | 1325 |
| QY | 1751 | tttgaatcggtttgagacacacttgctataagaaagaatgaaactttgaaagatctctgtgccg | 1810 |
| DB | 1326 | tatggaatgcgcgtcgaatgttagacaacagtgggacaatgatattacagatgattcatctgacg | 1385 |
| QY | 1811 | agcaatcagctctcttaaccgccttgtagcactgtgaaaggttggagaggaattgtgtgaaagc | 1870 |
| DB | 1386 | gacgtatcatctcaacaaactaga-----gcgggaagaagcatctgtttgtgacg | 1433 |
| QY | 1871 | tttcacgaatttgaacaagaaggccaacgcgtcatatcagttgaggaattatgacaga | 1930 |
| DB | 1434 | gttcaaatatttcttcaaaagaatgaaagcggttctatacaaatattatgacttaacaaagc | 1493 |

| | | |
|--------|--|------|
| b7 | agaaatccagcccccacacacagccttctgagccctcggaaagcggaggaagagagagagagagagagcctgcttgcgaacagc | 1870 |
| Db | gacgctccatctccacaacaactaga-----gcgggaagaagagatctctgttcgacg | 1433 |
| Q7 | tttcacgaatttgcacaagaaggcgcaacccgctatatcagctcgaagaattatgcacaaga | 1930 |
| b13434 | gttcaatattttgcacaagaatgaagagggtttcatatacaattatgatgcacaacagc | 1493 |


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QY 1931 ataaattctgtcccaactcattaccatcgcttcaagactgatacgaataatccgatgg 1990
DB 1494 gttgttgtaacatgagatggctgtgtttctccttgaagacatcatcaagaagtgtatca 1553
QY 1991 caa 1993
DB 1554 aaa 1556

RESULT 7
AAF74276
ID AAF74276 standard; DNA; 2251 BP.
XX
XX AAF74276;
AC
XX
XX 04-MAY-2001 (first entry)
DT
XX
DE Tobacco calcium dependent protein kinase clone.
XX
XX Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX
XX Nicotiana tobaccum.
OS
XX WO200107592-A2.
XX
XX 01-FEB-2001.
PD
XX 26-JUL-2000; 2000WO-GB02876.
PF
XX 27-JUL-1999; 99GB-0017642.
PR
XX
XX (ZENE) ZENECA LTD.
PA
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
XX WPI; 2001-168549/17.
DR
XX
XX Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX
XX Claim 18; Page 38-39; 50pp; English.
PS
XX
XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX
XX Sequence 2251 BP; 743 A; 371 C; 537 G; 598 T; 2 other;

Query Match 10.2%; Score 243.2; DB 22; Length 2251;
Best Local Similarity 54.2%; Pred. No. 2.1e-40;
Matches 538; Conservative 0; Mismatches 448; Indels 6; Gaps 2;
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RESULT 8
AAC42353
ID AAC42353 standard; DNA; 1761 BP.
XX
XX AAC42353;
AC
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XX 17-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 35231.
DE
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX
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PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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DT 18-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
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OS Arabidopsis thaliana.
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XX 01-FEB-2001.
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XX 26-JUL-2000; 2000WO-GB02876.
XX
XX 27-JUL-1999; 99GB-0017642.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Holt CD, White AJ, Michael AJ, Osborn RW;
XX WPI: 2001-168549/17.
XX
XX Producing herbicide resistance plants by inhibiting calcium dependent
XX protein kinase in plants or by providing an intracellular vacuolar
XX transporter capable of transporting agrochemical into plant vacuole
XX
XX Claim 18; Page 40; 50pp; English.
XX
XX The present invention describes a method of producing plants which are
XX resistant to the herbicides paraquat and diquat, involving inhibiting in
XX the plants a calcium dependent protein kinase (CDPK) and selecting those
XX plants which are resistant to the agrochemical of interest. This is
XX useful in the production of crops with herbicide resistance.
XX
XX Sequence 2040 BP; 586 A; 415 C; 513 G; 526 T; 0 other:

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Query Match          9.7%; Score 229.4; DB 22; Length 2040;
Best Local Similarity 58.6%; Pred. No. 1.3e-37;
Matches 417; Conservative 0; Mismatches 291; Indels 3; Gaps 1;

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Oy 798 gccgtcaagatcatgccaaagtaagatgacacggaataatccattgagatgttcgt 857
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Db 566 cggagatcatcagatcatcagacactatctggacacaaacatttgcagttccgggga 625

Oy 918 gaattggaagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 977
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Db 626 gcatctggaggaagaagacatgttccatgttgcattgagagcttcgcgtgctggggagcgc 685

Oy 978 ctagacagaataatagcagagcgaggagatacacagaggaagatgccaagcgatgtt 1037
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Oy 1038 gtaacgattttagagcgtatgacgtcttcacatcttcagaggggtagtcgcatgttattg 1097
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Db 743 agggcagctggttaagctgttcaacatttgcacatttaltatgagatgagatcgtgatttg 802

Oy 1098 aagccagaggaattcctcttccacaacagggatgaaatgcccacatgagttgattgat 1157
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Db 803 aaaccgaggaactcttacttgcacaacaaagaagaagatgctcacaagccaatgatt 862

Oy 1158 ttgtgctctctgatttcatatgacagaatgaaaggctaatgatatgttctgaaagtga 1217
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Db 863 ttgtgctcctcagtttcatatgaaagaagaaatgataagagacattgttggagtgct 922

Oy 1218 tatattgttccccagaggttttacacagatcatatagatgtaagcagaatcttggagtt 1277
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Db 923 taattatgttgcctcgaagctccttcgaggaattatgttaagaagatgatglatgaggt 982

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Db 983 gcaagcgctattatttgaacattcttcacagtggtgtctccacatttgggctgaaacatga 1042

Oy 1338 tcaggaatatctcgaatctgtgtgtgagagctgataccaaattgatgattcacacggtgct 1397

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Db 1043 aaggaataatttgatgctattcttccaagggagatgacttgagagltcaaccatgcca 1102
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Db 1163 agaattractcgcccaagttctccaacatcccttgctcagagatgagaa 1213

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RESULT 13

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AAAF74270
ID AAF74270 standard; DNA; 1791 BP.
XX
XX AAF74270;
XX
XX 04-MAY-2001 (first entry)
XX
XX Carrot calcium dependent protein kinase clone.
XX
XX
XX Calcium dependent protein kinase; CDPK; herbicide resistance;
XX paraquat; diquat; crop production; ds.
XX
XX Daucus carota.
XX
XX MO200107592-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-GB02876.
XX
XX 27-JUL-1999; 99GB-0017642.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Holt CD, White AJ, Michael AJ, Osborn RW;
XX WPI: 2001-168549/17.
XX
XX
XX Producing herbicide resistance plants by inhibiting calcium dependent
XX protein kinase in plants or by providing an intracellular vacuolar
XX transporter capable of transporting agrochemical into plant vacuole
XX
XX Claim 18; Page 34-35; 50pp; English.
XX
XX The present invention describes a method of producing plants which are
XX resistant to the herbicides paraquat and diquat, involving inhibiting in
XX the plants a calcium dependent protein kinase (CDPK) and selecting those
XX plants which are resistant to the agrochemical of interest. This is
XX useful in the production of crops with herbicide resistance.
XX
XX Sequence 1791 BP; 554 A; 286 C; 448 G; 503 T; 0 other:

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Query Match          9.4%; Score 224.2; DB 22; Length 1791;
Best Local Similarity 53.1%; Pred. No. 1.5e-36;
Matches 528; Conservative 0; Mismatches 456; Indels 9; Gaps 2;

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Oy 906 aaattctatgatgcattgtagagatggtcctcaatgctacatgtgcatggaattatgtgag 965
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Db 521 gattttaaagtgctttttagagataggcaatctgtgcaccttgatgagagcttltgtct 580

Oy 966 gaggagaatttgcctagacagaatattagccagaggggagataccagaagaagtgc 1025
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Db 581 gcttgaggagctgttgcacaggaattacagctcaa--ggacattaccctggaagagagcgct 637

Oy 1026 aagcattgtgttacagattttagagcgtagtagcctctgtcatcttcaagggttagtg 1085

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| XX | 06-SEP-2000. | |
| XX | | |
| XX | 25-FEB-2000. | 2000SEP-0301439 |
| XX | | |
| XX | 25-FEB-1999. | 9905-0121825 |
| PR | 09-MAR-1999. | 9905-0123180 |
| PR | 23-MAR-1999. | 9905-0123548 |
| PR | 25-MAR-1999. | 9905-0125788 |
| PR | 29-MAR-1999. | 9905-0126785 |
| PR | 01-APR-1999. | 9905-0127462 |
| PR | 08-APR-1999. | 9905-0128234 |
| PR | 16-APR-1999. | 9905-0128714 |
| PR | 19-APR-1999. | 9905-0129645 |
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| PR | 04-MAY-1999. | 9905-0132484 |
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| PR | 06-MAY-1999. | 9905-0132486 |
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| PR | 07-MAY-1999. | 9905-0132683 |
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| PR | 19-MAY-1999. | 9905-0135441 |
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| PR | 25-MAY-1999. | 9905-0136021 |
| PR | 27-MAY-1999. | 9905-0136392 |
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| PR | 01-JUN-1999. | 9905-0137222 |
| PR | 03-JUN-1999. | 9905-0137528 |
| PR | 04-JUN-1999. | 9905-0137602 |
| PR | 07-JUN-1999. | 9905-0137724 |
| PR | 08-JUN-1999. | 9905-0138094 |
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| PR | 23-JUN-1999. | 9905-0140353 |
| PR | 23-JUN-1999. | 9905-0140354 |
| PR | 24-JUN-1999. | 9905-0140695 |
| PR | 28-JUN-1999. | 9905-0140823 |
| PR | 29-JUN-1999. | 9905-0140991 |
| PR | 30-JUN-1999. | 9905-0141287 |
| PR | 01-JUL-1999. | 9905-0141842 |
| PR | 01-JUL-1999. | 9905-0142154 |


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Db      508  gttgggagtgcttattacacgcacctgagggttttgaaaagaagatgaccagagca 567
Oy      1266  gaacatttgagatgaagtgatcaacgatactctgctgtagcgagtcgcatcttg 1325
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Oy      1446  gattacgcgcaaaagaatgacgctgttcaacgactgaactacactcttggtgtagaag 1505
Db      748  gatccaaagaagaactaactgctgctcaagttctcaaccatccatgagatcaaggagat 807
Oy      1506  caaaggc-----agatcccgctggaatatactatcttcagatlaaagcaatacctc 1559
Db      808  gggagggcaccagatgttccctctgtaatacggtgtagtccaggtcccaacaatccaaa 867
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Oy      1620  gaactttgatactcaaacgtagttaaactgctcgaacctgagagatggtgtgtatca 1679
Db      928  gaatcatatgggttgagaagagatgtttaaagtgatctgatactgtagtgaacaact 987
Oy      1680  ctgacaactcttcgagcggcactaacgcgatatattactgagtctatgaaggaaatcgagg 1739
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Db      1108  ttatctgcagcccaatgcatatcaacaagaacttga-----cagaagaagaacat 1155
Oy      1860  gctggaacagcttccagcaatctgacaagaaggagcaaccgagatcatatcagttgagaa 1919
Db      1156  cttaactcagccttccacaaccttgcacaagaagacaagatgtagatatacacaatggagag 1215
Oy      1920  ttgacacagaagatca 1934
Db      1216  ctgagagcaagcccta 1230

RESULT 15
AAV36878
ID      AAV36878 standard; cDNA; 1020 BP.
XX
AC      AAV36878;
XX
DT      12-OCT-1998 (first entry)
XX
DE      Nucleotide sequence of ATCDPK1a PK domain.
XX
KW      ATCDPK1a; protein kinase; PK; tolerance; drought; salinity; cold; heat;
XX      fruit; ornamental; vegetable; cereal; field crops; ds.
XX
OS      Arabopsis sp.
XX
FH      Key Location/Qualifiers
FT      CDS 97..918
FT      /tag= a
FT      /product= "ATCDPK1a PK protein"
FT      /note= "no stop codon specified"
XX

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PN      W09826045-A1.
XX
PD      18-JUN-1998.
XX
PF      12-DEC-1997; 97WO-US23019.
XX
PR      13-DEC-1996; 96US-0032966.
XX
PA      (GENO ) GEN HOSPITAL CORP.
XX
PI      Sheen J;
XX
DR      WPI; 1998-348509/30.
XX
DR      P-PSDB; AAM49837.
XX
PT      Protecting plants against environmental stress - by introducing
PT      protein kinase domain-containing gene, calcium dependent protein
PT      kinase gene or calcium/calmodulin-dependent gene
XX
PS      Claim 17; Fig 5; 62pp; English.
XX
CC      This is the nucleotide sequence of the ATCDPK1a protein kinase (PK)
CC      domain isolated from the Arabopsis cDNA library, and used in the method
CC      of the invention to protect plants against environmental stress. The
CC      methods can be used for improving the tolerance of plants to
CC      environmental stresses such as drought, salinity, cold and heat. They
CC      provide for increased production efficiency, as well as for improvements
CC      in quality and the yield of crop plants and ornamentals. The methods
CC      contribute to the production of high quality and high yield agricultural
CC      products, e.g. fruits, ornamentals, vegetables, cereals, and field crops.
XX
Sequence 1020 BP; 265 A; 194 C; 280 G; 277 T; 4 other;
XX

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Query Match 9 38; Score 219.8; DB 19; Length 1020;
Best Local Similarity 57.48; Pred. No. 1e-35;
Matches 417; Conservative 0; Mismatches 307; Indels 3; Gaps 1;

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Db      206  tagcttgcaaatcaatctccaaagagaagtcgccagcgcgtcgatgtgaaagctcc 265
Oy      856  gttagaagaatlaaaattttgaagcggtatcaggggcaacaaatctcgtcaaatctatg 915
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 Db 863 agcgtttgactgtctcagcaagttcttgatcaccccttgatacagaatgcagaagaaagaa 922
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 Db 923 tcaagct 929

Search completed: May 2, 2002, 06:30:00
 Job time: 6540 sec

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Db 439 GAGCCCCAAAAAATGAGATATAAATCGGAGCCGGCTACTACATTCGCCCTGAGGTG 498
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Qy 1239 ctgctcttgccagtcggccattctcggcacagacagatcagagatattccgactctg 1358
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Qy 1479 ctgaactcacttggt 1495
Db 739 TTAGATCATCATGAT 755

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RESULT 4

US-08-338-057-1

Sequence 1, Application US/08338057

Patent No. 5795741

GENERAL INFORMATION:

APPLICANT: Tomley, Fiona M.

APPLICANT: Dunn, Paul P. J.

APPLICANT: Bumstead, Janene M.

APPLICANT: Vermeulen, Arno N.

TITLE OF INVENTION: Coccioidosis poultry vaccine

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Organon Teknika Corporation

STREET: 1330 Piccard Drive

CITY: Rockville

STATE: Maryland

COUNTRY: U.S.A.

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/338,057

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93.30907.9

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Gormley, Mary E.

REGISTRATION NUMBER: 34,409

TELEPHONE: (301) 258-5200

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1400 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: C-terminal

ORIGINAL SOURCE:

ORGANISM: Elmeria maxima

STRAIN: Houghton

DEVELOPMENTAL STAGE: sporozoite

IMMEDIATE SOURCE:

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LIBRARY: sporozoite cDNA cloned in Lambda ZAP11
CLONE: Em/0-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-338-057-1

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Query Match 6.4%; Score 153; DB 1; Length 1400;
Best Local Similarity 52.4%; Pred. No. 2.8e-25;
Matches 386; Conservative 0; Mismatches 345; Indels 6; Gaps 2;

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Qy 759 ggcgtcgtaagaaggcgagttacaaaggacagccgcgcgtcaagatcgcga 818
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Db 202 TTTTATCTTGTTCACGAGATATATACAGGAGGAGAAATTAATTTGATGAATTAATCA 261
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Db 739 TTAGATCATCATGAT 755

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RESULT 5

US-08-668-416-1

Sequence 1, Application US/08668416

Patent No. 5843722

GENERAL INFORMATION:

APPLICANT: Tomley, Fiona M.

APPLICANT: Dunn, Paul P. J.

APPLICANT: Bumstead, Janene M.

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-07-951-715A-20

Query Match 6.4%; Score 151.6; DB 1; Length 1349;
Best Local Similarity 53.9%; Pred. No. 5,6e-25;
Matches 335; Conservative 0; Mismatches 284; Indels 3; Gaps 1;
QY 883 tatcaggacacataatctcgtcaaatctatgatgcatgtgagatgagcctcaatgctc 942
DB 19 TCTCGCGCCAGCCCAACGTCGTGGCTCCGCCCGCTACGAGACAGCAAGAGCGTGC 78
QY 943 acattgtcatgaaatattgtgagagagaaattgctagacagaaatattagccaagagcg 1002
DB 79 ACCGTGCTATGAGAGCTGTCGGCGGGGAGAGCTTTCAGCCGATCATTCGCCGGGGCC 138
QY 1003 ggaatataccagagaaagtgtccaaagagatgtgttctacagattttgagcgtgtagcct 1062
DB 139 AG---TACACGAGAGCGCGCGCGCGAGCTGCTGCCGCATCGTCAGATGTCACAA 195
QY 1063 tctgtcatcttcaggagagtagtgcgtgatttgaagccagagaaattccctttacaa 1122
DB 196 CTTGCCACATCCATGGGGGATGACACCGGACATCAAGCCCGAGAACTTCTCTCTCA 255
QY 1123 ccaggagatgaaatgctcccatgaaattgattgttctctctgatttcattatgac 1182
DB 256 GCAAGGACGAGACCGCGCTCAAGGACGACACTTCGCGCTCTCCGCTTCTTCGAAG 315
QY 1183 cagatgaaaggttaatgattgttgaagtgcataatatgttgcagagaggtttac 1242
DB 316 AGGGGAGCTGTCAGGGGACATGTCGAGCGCTACTACATCAATCGGCGCCGAGTCTCA 375
QY 1243 acaagatcatatagtagtgaagcagacatttggagtagtgcataaagtaattcctc 1302
DB 376 AAGAGAAAGTACGCGCCGAGGCGGACATCTGAGCGCTCGGCTCATGCTTACATCTTCC 435
QY 1303 tctgtgcaagtcgagcattctgggacagacagaaatcagaaatattcctatctgtgtga 1362
DB 436 TCGCGCGGCTGCTCCCTTCTGGGAGAGAGAGAGCATCTTCACCGCGCATCTCG 495
QY 1363 gagctgattcccaacttgaattcaacgctggcctacagatcatcagctgaagtaagatt 1422
DB 496 GAGGGCAGCTTACCTCTCCACGCGAGCCATGCGCACACATCTCGCGGAGCAAGATC 555
QY 1423 ttgtgaagaagattctgaaacaaagattaccgaaagaatgacgctgttcaagacctga 1482
DB 556 TCGTCAAGAAAGTGTCTCAACATCAACCCCAAGAGCGGCTTCAGCGCTTCCAGGTCTCA 615
QY 1483 ctcatccttgtgtcgagatga 1504

Db 616 ATCACCCTGATCAAGAGAA 637
|||||
RESULT 7
US-08-459-448A-20
Sequence 20, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Kozielec, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlino, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-08-459-448A-20

Query Match 6.4%; Score 151.6; DB 2; Length 1349;
 Best Local Similarity 53.9%; Pred. No. 5,6e-25;
 Matches 335; Conservative 0; Mismatches 284; Indels 3; Gaps 1;

QY 883 taccagggacacaataatcctgcgaatctatgatgcatgtaggaatggcctcaatgctc 942
 DB 19 TCTCCGGCAGCCCAACGTGTGGGCTCCGGGGCGGTACAGAGCAAGAGAGGTGC 78
 QY 943 acattgcatggaattatgtaggaagaagaattcttagacagaatattagccaagagcg 1002
 DB 79 ACCTGTGTATGAGGTGTGGGGGGGGGAGCTCTTCCAGCCGATCATCGCCGGGGCC 138
 QY 1003 ggaagatacaagaagaatgccaagaagcattgctgacagattttgagcgttagacct 1062
 DB 139 AG---TACACGAGAGCGCGCGCGCGGAGCTCTCGCGCCCATCGTCGATCGTCACA 195
 QY 1063 tctgtcatcttcaaggagtagtgcacatgtaatttgaagccaagaatttcctttcaca 1122
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 QY 1123 ccaggatgaagaatgctcccaagaattgattgatttggctctcctgattcattagac 1182
 DB 256 GCAAGAGCAGAGAGCGCGCGCTCAAGCCACCGACTTCGGCTTCCTTCCTTCAAGG 315
 QY 1183 cagatgaagagcttaatatgttgaagtgatcatattatgttgcacagaaggtttac 1242
 DB 316 AGGGGAGCTGCTCAGGAGCATCGTCGAGCGCCTACTACATCGCGCCGAGGTCTCA 375
 QY 1243 acagatcatatagtagtgaagcagaacatttgaagtagataggtgtcacaacgtacatctgc 1302
 DB 376 AGAGGAATACGCGCCCGGAGCGGACATCTGAGCGCTCGGCTCATGCTTCACTCTTC 435
 QY 1303 tctgagcagctggcattcttgagcagaacagaatcagaatattccgattctgttga 1362
 DB 436 TCGCCGGGCTGCTCTCTTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
 QY 1363 gagctgcatcccaactttgtagtcaacgctggcctacagtagtcaagctgaagatt 1422
 DB 496 GAGGGAGCTTACCTCTCCACGAGCCATGGCCACACATCTCGCGGAGGACCAAGATC 555
 QY 1423 ttgtgaagagatttctgaacaagaatttacgcaaaagaatgacgctgttcaagcactga 1482
 DB 536 TCGTCAAGAGATGCTCAACATCAACCCCAAGAGGCGCTCAAGGCTCTCAAGTCTCTCA 615
 QY 1483 ctcatccttggttcgagatga 1504
 DB 616 ATCACCACATGATCAAGAAGA 637

RESULT 8

US-08-459-595A-20

Sequence 20, Application US/08459595A

Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Ewola, Stephen V.

APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlino, Ellis J.

APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6018104artis Corporation
 STREET: Patent & Trademark Dept., 520 White Plains
 STREET: Rd., POB 2005
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,595A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIY3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note="cDNA sequence for maize

OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as

OTHER INFORMATION: disclosed in Figure 30."

US-08-459-595A-20

Query Match 6.4%; Score 151.6; DB 3; Length 1349;

Best Local Similarity 53.9%; Pred. No. 5,6e-25;

Matches 335; Conservative 0; Mismatches 284; Indels 3; Gaps 1;

QY 883 taccagggacacaataatcctgcgaatctatgatgcatgtaggaatggcctcaatgctc 942
 DB 19 TCTCCGGCAGCCCAACGTGTGGGCTCCGGGGCGGTACAGAGCAAGAGAGGTGC 78
 QY 943 acattgcatggaattatgtaggaagaagaattcttagacagaatattagccaagagcg 1002
 DB 79 ACCTGTGTATGAGGTGTGGGGGGGGGAGCTCTTCCAGCCGATCATCGCCGGGGCC 138
 QY 1003 ggaagatacaagaagaatgccaagaagcattgctgacagattttgagcgttagacct 1062
 DB 139 AG---TACACGAGAGCGCGCGCGCGGAGCTCTCGCGCCCATCGTCGATCGTCACA 195
 QY 1063 tctgtcatcttcaaggagtagtgcacatgtaatttgaagccaagaatttcctttcaca 1122
 DB 196 CCGTGCACCTCCATGGGGGATGACACCGGACATCAAGCCGGAACCTTCGTCTCTCA 255
 QY 1123 ccaggatgaagaatgctcccaagaattgattgatttggctctcctgattcattagac 1182
 DB 256 GCAAGAGCAGAGAGCGCGCGCTCAAGCCACCGACTTCGGCTTCCTTCCTTCAAGG 315

| | | | |
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| QY | 1183 | caagatgaaggcttaacgatgatctgttggaagatgcataatgtgtgtcccaagaggtttac | 1242 |
| Db | 316 | AGGGGAGACCTCTAAGGAGACATCGTGGCAGGCCCTACTACATCGCGCCGAGGGTCTCA | 375 |
| QY | 1243 | acagatcatatagatatygaagcagaaatttgtagtataagtgltcatalaagctacatctgc | 1302 |
| Db | 376 | AGAGAGAGTACGGCCCGGAGGCCGACATCTGGAGGCTCGGCTCATAGCTCATCTTC | 435 |
| QY | 1303 | ctcttgagcagtcgagccattctggcagcaagaaatcagaaatattccgattctgtgtga | 1362 |
| Db | 436 | TGCGCGGGGCGCCCTCTTGGGGAGAGAGACGATCTTTCACGCGCATCTTCG | 495 |
| QY | 1383 | gagcttgatcccaacttttgatgatccgttgacctacagtatcaagctgaagtaaagat | 1422 |
| Db | 496 | GAGGGCAGCTTGACCTCTCCAGCGAACCATTGGCCACATCTTCGCGGGAGGCAAGGATTC | 555 |
| QY | 1423 | ttgtgaagagatattctlgaaacaaagattaccgcaaaagaaatgaacgctgttcaagacatga | 1482 |
| Db | 556 | TGCTGACGAGAGATGCTCAACATCAACCAACCCAGAGAGGGGCTCATCGGCGTTCCAGAGTCTCA | 615 |
| QY | 1483 | ctcatccttggttgcgagatga | 1504 |
| Db | 616 | ATCACCCATGATCAAGAAGA | 637 |

RESULT 9
 US-08-459-504B-20
 : Sequence 20, Application US/08459504B
 : Patent No. 6075185
 : GENERAL INFORMATION:
 : APPLICANT: Kozziel, Michael G.
 : APPLICANT: Desai, Nallni M.
 : APPLICANT: Lewis, Kelly S.
 : APPLICANT: Kramer, Vance C.
 : APPLICANT: Warren, Gregory W.
 : APPLICANT: Evola, Stephen V.
 : APPLICANT: Crossland, Lyle D.
 : APPLICANT: Wright, Martha S.
 : APPLICANT: Merlin, Ellis J.
 : APPLICANT: Launis, Karen L.
 : APPLICANT: Rothstein, Steven J.
 : APPLICANT: Bowman, Cindy G.
 : APPLICANT: Dawson, John L.
 : APPLICANT: Dunder, Erik M.
 : APPLICANT: Pace, Gary M.
 : APPLICANT: Suttle, Janet L.
 : TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 : INSECTICIDAL ACTIVITY IN MAIZE
 : NUMBER OF SEQUENCES: 94
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: No. 6075185artis Corporation
 : STREET: 3054 Cornwallis Road
 : CITY: Research Triangle Park
 : STATE: NC
 : COUNTRY: USA
 : ZIP: 27709
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: PC-DOS/MS-DOS
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/459,504B
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/459,595
 : FILING DATE: 02-JUN-1995
 : APPLICATION NUMBER: US 07/951,715
 : FILING DATE: 25-SEP-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/772,027
 : FILING DATE: 04-OCT-1991

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? ATTORNEY/AGENT INFORMATION:
? NAME: Meigs, J. Timothy
? REGISTRATION NUMBER: 38,241
? REFERENCE/DOCKET NUMBER: CGC1577/CIF/DIV
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (919)541-8587
? TELEFAX: (919)541-8689
? INFORMATION FOR SEQ ID NO: 20:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1349 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHEICAL: NO
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 3..1226
? OTHER INFORMATION: /note="cDNA sequence for maize
? OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
? OTHER INFORMATION: disclosed in Figure 30."
US-08-459-504B-20

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| Query Match | 6.4% | Score 151.6 | DB 3 | Length 1349 |
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| Best Local Similarity | 53.9% | Pred. No. 5.6e-25 | | |
| Matches 335 | Conservative 0 | Mismatches 284 | Indels 3 | Gaps 1 |
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| QY 943 | acatgtcatgaatatagtgtagggaggaagatgtcttagacgaatatatagccaaagcgc | | | 1002 |
| Db 79 | ACCTCGTATGAGCTGTGCGCGGGGGAGACTTTTGACACCGCATCATGCGCGGGGCGC | | | 138 |
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| QY 1123 | ccagaggatgaanaatcgtcccatgaagtgtgattgtattgtgtctctgtatctcatagac | | | 1182 |
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| QY 1183 | cagatgaaggctcaatgatatatgttttgaagtgcatatlatgtgtgcccagaagtttac | | | 1242 |
| Db 316 | AGGGCGAGCTCCTCAGGACATCGTCGGCACCGCTTACATATGGCCGCCACAGGCTCA | | | 375 |
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| Db 376 | AGAGGAGTACGAGCGCCCGAGGCGCCACATCTTGAGCGCTGCGGTCACTTACATCTTCC | | | 435 |
| QY 1303 | tcgttgacgtcggccatctctggcgacgaaagaataatcagaataatccgactgtgtga | | | 1362 |
| Db 436 | TCCGCGCGCGTCCCTCTTCTTGCGCAAGAACGAAACGGCATCTTCAACCCCATCTCCG | | | 495 |
| QY 1363 | gaagtgatcccaacttttgatgatcatcacggtgctacagtatcaagtctgaagttaagatt | | | 1422 |
| Db 496 | GAGGGCAGCTTGACCTCTCCAGCGAGCGCATGGCCACATCTGCCGGGACCAAGGATC | | | 555 |
| QY 1423 | ttgtgaagaatattcttgaacaaagattaccgcaaaagaatgacgcgtgttcaacacgta | | | 1482 |
| Db 556 | TTCGTCAGAGAGATGCTCAACATCAACCCCAAGAGCGGCTCAGCGCTTCCAGGTCTCA | | | 615 |
| QY 1483 | ctatcacttggttgcgagatga 1504 | | | |
| Db 616 | ATACACCATGATCAAGAGA 637 | | | |

APPLICANT: Evola, Stephen V.
 APPLICANT: Crossland, Lyle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merrill, Ellis J.
 APPLICANT: Launis, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dundee, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttle, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5859336artis Corporation
 STREET: Patent & Trademark Dept., 520 White Plains
 STREET: Rd., POB 2005
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591-9005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,448A
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Pace, Gary M.
 REGISTRATION NUMBER: 40403
 REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIVA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8682
 TELEFAX: (919)541-8689
 INFORMATION FOR SRO ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4162 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
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 NAME/KEY: misc_feature
 LOCATION: 1418..1427
 OTHER INFORMATION: /note="start of mRNA"
 FEATURE:
 NAME/KEY: exon
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 NAME/KEY: Intron


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OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
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FEATURE:
NAME/KEY: Promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-595A-26

Query Match 6.0%; Score 143; DB 3; Length 4162;
Best Local Similarity 53.6%; Pred. No. 7.6e-23;
Matches 349; Conservative 0; Mismatches 290; Indels 12; Gaps 2;

QY 680 cgggtctcgaagaactcgcgcgaagtagagctcgggaaggcggggagggccca 739
DB 1729 CCGGCCCATGAGAGACGTCGCGGCACTCTCGATGGGCAAGGAGCTCGGCGGCGCA 1788
QY 740 ctccgacacactctcgcgcgtctcgaagaaggcgaagtagacagacacgtcgc 799
DB 1789 GTTCGGCGTGAAGCAGCTGTGCACGACCGGAGCGAGC-----GGCAGAGAGCTGGC 1839
QY 800 cgtcaagctctcgcgaagaagtagagtagacagcgaatcatcattgagagtag 859
DB 1840 GTGCAAGACGATCGCGAAGCGGAAGCTGCGCGCAGGAGAGCGAGAGCTGCGCGC 1899
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DB 1900 GGAGGTGAGATCATGACCCACTCTCCGGCCACCCCAACGTGGTGGGCTCCGCGGCGC 1959
QY 920 atgtgagatgagcctcatatgtcatatgtgaattatgagagagagagatgct 979
DB 1960 GTACGAGAGACAAAGACGCGTGCACCTCTCATGAGAGCTGTGCGCGGCGGAGACTCTT 2019
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QY 980 agacagaatattagccagagcgggagatacacagaggaagatgccaaagcattgtgt 1039
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QY 1040 acagattttagcgtagtagccttctgtcatcttcgaagggttagtcatctgtattgaa 1099
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QY 1100 gccagaagaattctcttcaacacagaggaatgaatgtcccatgaagttagtattt 1159
DB 2137 GCCGAGAACTTCTCTGTGTGTCAGAGAGAGAGAGAGCCCTCAAGGCCACCACTT 2196
QY 1160 tggctctctgtattcaatgaccagatgaagccttaatgatattgttgaagtgcata 1219
DB 2197 CGGCTCTCTCGCTCTCTCAAGAGAGGCGGAGCTGTACAGGACATCGTGGAGCGCTA 2256
QY 1220 ttatgttccccagaggttttacagagatcatatagtagaagcagacatttgagtat 1279
DB 2257 CTACATCGCGCCCGAGGTGCTCAAGAGAGAGAGAGAGCCCGGAGCGGACATCTGGAGCGT 2316
QY 1280 aggtgtcaataacgtacattctgtctgtgcaagtcgagcattctgggcaag 1330
DB 2317 CGGCGTCATGCTCTCATATCTTCTCGCGGCGGCTGCTCCCTTGGGCAAG 2367

RESULT 14
US-08-459-504B-26
Sequence 26, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nallni M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6075185artle Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
```


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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 2, 2002, 04:38:15 ; Search time 2003.89 Seconds
(without alignments)
12730.478 Million cell updates/sec

Title: US-09-854-731-3
Perfect score: 2374
Sequence: 1 gcacagggcgatccgacat.....ccacatccccccctcagcg 2374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues
Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estom:*
5: em_estpl:*
6: em_estro:*
7: em_estov:*
8: em_hc:*
9: em_hc:*
10: gp_est1:*
11: gp_est2:*
12: gp_hc:*
13: gp_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 522.8 | 22.0 | 851 | 10 | AM48132 BRY_1726 |
| 2 | 478 | 20.1 | 597 | 10 | AM257900 687063G05 |
| 3 | 454.4 | 19.1 | 562 | 11 | BF422010 FMI_11.G0 |
| 4 | 386 | 16.3 | 491 | 10 | BE590469 WHE0854.F |
| 5 | 365.8 | 15.4 | 655 | 10 | AM685958 NF032B08N |
| 6 | 363 | 15.3 | 622 | 11 | BF520876 EST458349 |
| 7 | 357.2 | 15.0 | 758 | 11 | BG592840 EST491518 |
| 8 | 356.6 | 15.0 | 557 | 11 | BG357062 OV2_9_D12 |
| 9 | 353.8 | 14.9 | 743 | 11 | BG351862 135B07 Ma |
| 10 | 337.2 | 14.2 | 491 | 11 | T18715 5C04G11-T7 |
| 11 | 333.6 | 14.1 | 575 | 11 | BF421980 FMI_11.G0 |
| 12 | 333.6 | 14.1 | 653 | 10 | AT487355 EST245677 |

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|----|-------|------|-----|----|----------|
| 13 | 332 | 14.0 | 653 | 10 | AT489424 |
| 14 | 325.4 | 13.7 | 551 | 10 | AM688043 |
| 15 | 321.8 | 13.6 | 326 | 10 | AU032386 |
| 16 | 321 | 13.5 | 644 | 11 | BE942153 |
| 17 | 314.8 | 13.3 | 597 | 10 | AV833696 |
| 18 | 311.2 | 13.1 | 382 | 11 | T18633 |
| 19 | 307.2 | 12.9 | 571 | 10 | AT759795 |
| 20 | 302 | 12.7 | 602 | 10 | AT774674 |
| 21 | 297.6 | 12.5 | 576 | 10 | AT487605 |
| 22 | 295.4 | 12.4 | 460 | 10 | AM930981 |
| 23 | 293.6 | 12.4 | 544 | 10 | AT759787 |
| 24 | 292.2 | 12.3 | 357 | 10 | AM324597 |
| 25 | 283.8 | 12.0 | 671 | 11 | BG126719 |
| 26 | 282.8 | 11.9 | 669 | 11 | BG126958 |
| 27 | 281.4 | 11.9 | 666 | 11 | BG447969 |
| 28 | 280.8 | 11.8 | 532 | 11 | BG790072 |
| 29 | 280.4 | 11.8 | 707 | 11 | BF292168 |
| 30 | 272.6 | 11.5 | 474 | 10 | BE056312 |
| 31 | 267.4 | 11.3 | 562 | 10 | AT166280 |
| 32 | 266 | 11.2 | 656 | 10 | BE317046 |
| 33 | 266 | 11.2 | 659 | 11 | BF595411 |
| 34 | 261.4 | 11.0 | 618 | 11 | BF595411 |
| 35 | 259.8 | 10.9 | 590 | 11 | BT422962 |
| 36 | 257.8 | 10.9 | 680 | 11 | BG586813 |
| 37 | 251.8 | 10.6 | 416 | 10 | AV428222 |
| 38 | 251.2 | 10.6 | 498 | 10 | AM030900 |
| 39 | 250.2 | 10.5 | 678 | 11 | BT208239 |
| 40 | 242.4 | 10.2 | 640 | 10 | AM033249 |
| 41 | 240.2 | 10.1 | 626 | 10 | AM775106 |
| 42 | 235.6 | 9.9 | 702 | 10 | AM565870 |
| 43 | 235 | 9.8 | 423 | 11 | C22392 |
| 44 | 233.2 | 9.8 | 599 | 11 | BF638757 |
| 45 | 228.4 | 9.6 | 697 | 11 | BG356745 |

ALIGNMENTS

RESULT 1
LOCUS AM48132 851 bp mRNA EST 03-JAN-2001
DEFINITION BRY_1726 BRY Trilicium aestivum cDNA clone P46-11G, mRNA sequence.
ACCESSION AM48132
VERSION AM48132.1 GI:12018793
KEYWORDS EST.
SOURCE Trilicium aestivum
ORGANISM bread wheat.
REFERENCE 1 (bases 1 to 851)
AUTHORS Clarke,B.C., Hobbs,M. and Appels,R.
TITLE Genes active in developing wheat endosperm
JOURNAL Unpublished (2000)
COMMENT Contact: Bryan Clarke
Division of Plant Industry
C.S.I.R.O.
GPO Box 1600, Canberra, ACT, Australia
Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
Email: bryancepl@csiro.au.
FEATURES
source
1. 851
/organism="Trilicium aestivum"
/cultivar="Wuna"
/db_xref="taxon:4565"
/clone="P46-11G"
/clone_lib="BRY"
/cell_type="endosperm"
BASE COUNT 233 a 172 c 193 g 250 t 3 others
ORIGIN

Query Match 22.0%; Score 522.8; DB 10; Length 851;
 Best Local Similarity 84.3%; Pred. No. 1.1e-74;
 Matches 670; Conservative 0; Mismatches 115; Indels 10; Gaps 7;

QY 1110 ttcctttcacacacagagatgaataatgctccacgaagtatgattgattgctcctc 1169
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 Db 2 TTCCTTTTACAAACAGATGAATAATGCCCATGAATGATTGATTGGTCTCTCT 61

QY 1170 gatttcattagccagatgaagaagcttaagatattgtctgaagtgcataattgtgcc 1229
 |||||
 Db 62 GATTTCATCAGACGAGATGAAGGCTCAATATATTGGAAAGTCATATTATGTTGCC 121

QY 1230 ccaagagctttcacacagatcatatagtagtggaagcagacatttgagatagtgctata 1289
 |||||
 Db 122 CCAGAGGTTTACACAGATCATACAGTATGACAGACGACATTGGAGTATAGGTCTATA 181

QY 1290 acgtacattcgtcctgtgacagtcgcacattctgagcagcaagaatacagaatattc 1349
 |||||
 Db 182 ACATACATTCGCTCTGTGTAGTCGGCATTTTGGGACGACAGAACTCGAATCTTC 241

QY 1350 cgaatcgtgtggaagagctgacacattgattgattcaccgtgtgctacagatcagct 1409
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 Db 242 CGATTCGATTGACAGCTGATCCCACTTGATATTCACCATGCGCTTCAGTCTAGCT 301

QY 1410 gaagctaagagattctgtgaagaagattctgacacaaagattacccgaaagaatgacgct 1469
 |||||
 Db 302 GAAGCTAAGAGATTGTTGAAAGATTCTTAAACAGAGATTACCGCANAGATACAGCT 361

QY 1470 gttaagaagactgactcattcctgtgtgagagatgaacaaagagatccgcgtgagacata 1529
 |||||
 Db 362 GTCCAGGATTTGACTCACCTGTTGGTGGGATGACCAAGACAGATTCCGCTTGATATT 421

QY 1530 ctcatcttcagatattaaagaacataaccctcgcgctac-acctcttaacgcttgagct 1588
 |||||
 Db 422 CTGTCTACAGATTAATTAAGCATACCTTGCTGCTCACTCCCTTTAAAGCTTTGGCCT 481

QY 1589 aaa--ggcacatccaaagcctt--aagggaagaatgaactttgatacctcaaacctgagct 1644
 |||||
 Db 482 AAAAGGCGAATTATCCAAAGGCTTTTAAAGGATGATGAAGAACTTGATGCTTAAGCTACAG 541

QY 1645 ttaaacgctcgaacctagagatggtttgatacacttgacaacttcggaagagcactaa 1704
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 Db 542 TTGATCTGCTTGAACCTTAAATATGAGTGTGGTCACTTGGACACTTTCGACGCTTTAA 601

QY 1705 cgcgaatttaactgatagtcagaagaalcgagaggtcttgaaatttttcacgctt-9 1763
 |||||
 Db 602 CGCGGTTTCACTGATGATGATGAAGCAATCAAGAAATTCTTGAAGTTTTCATGCCCTTG 661

QY 1764 gaaccacttgacata-cagaaagaatggaacttgaaagattctgtgcccagacaatcagctc 1822
 |||||
 Db 662 GACCCACTTTCATACCGGAATATTGTTTCAAGAAATTTTGTGCCGACTTATTAGCCCC 721

QY 1823 ttaacagcttgagacacttga--aagtggaagagatg-gctggaacagcttcacagca 1879
 |||||
 Db 722 TTACCAAGTTTGAAGCCCTGACCAAGATTGGAAGAGAGATTGTTGGAACAACCTTTTACGA 781

QY 1880 atttgaacaagagg 1894
 |||||
 Db 782 CTTTGGAAACAGGAG 796

RESULT 2
 AM257900 597 bp mRNA EST 30-MAR-2000
 LOCUS 687063605.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA
 DEFINITION sequence.
 ACCESSION AM257900
 VERSION AM257900.1 GI:6626368
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

REFERENCE 1 (bases 1 to 597)
 AUTHORS Walbot V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 687063 row: G column: 05.
 Location/Qualifiers
 1..597
 /organism="Zea mays"
 /cultivar="Illinois High Oil"
 /db_xref="taxon:4577"
 /clone_lib="687 - Early embryo from Delaware"
 /issue_type="embryo"
 /dev_stage="14, 21, 28, and 35 days after pollination"
 /lab_host="E. coli SOLR"
 /note="Organ: embryo; Vector: pBluescript SK; Site_1: XhoI; Site_2: EcoRI; Library was prepared by Statagene using the Uni-ZAP XR system (Stratagene BN937328-12). Clones were picked by a Q-bot after blue/white selection (ampicillin resistance - use 100 micrograms/microliter). Developed from a pool of equal amounts of RNA from developing embryos sampled at 14, 21, 28 and 35 days after pollination of the Illinois High Oil Maize Strain Cycle 90. This closed strain has been selected for high oil concentration for 90 generations and originates from the 1890s era open pollinated variety Burr's White"

BASE COUNT 172 a 127 c 141 g 157 t
 ORIGIN

Query Match 20.1%; Score 478; DB 10; Length 597;
 Best Local Similarity 88.1%; Pred. No. 1.8e-67;
 Matches 520; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1371 cccaacttgatgattcaccgctgacctacagatagcgtgaagcgaatttgagg 1430
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 Db 7 CCCAATTTTACGATTTACACATGCGCTTCAATGCTGCTGAGGCTTAAGGATTTTGAAG 66

QY 1431 agattctgaacaaagattaccgcaaaagaatgacgcgtgttcaagcactgactcact 1490
 |||||
 Db 67 AGATTCTGTACAAAGATTACCGCAAAAGATGATGCTGCTCAAGCACTGACTCACCT 126

QY 1491 tggttgagagatgaacaaagagatcccgctgagacatactcattcaagattaataag 1550
 |||||
 Db 127 TGGTTACGAGATGAACAAAGCAAAATTCATTGACATCACTATTGTAAGTTTGAAG 186

QY 1551 caatacctccgcgtacacactcttaaacgctgtgacataaaggacataccaagcctta 1610
 |||||
 Db 187 CAGTATTCGCCGTACGCTACCTCTTAAGCTTTGGCATTAAGCGCATTTCTAAGCTTTA 246

QY 1611 agggaaagatgaactttgatactcaactgcaagtttaacgtgctcogaactagagatgg 1670
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 Db 247 ACGGAGATGAACCTTTGTATCTTGTGTTGCAAGTTTAAGCTTGAACCCAGAGATGG 306

QY 1671 ttgtatcaacttgacaacttcgagcgcacataagagatatctaactgatactatgaag 1730
 |||||
 Db 307 TTGCGTCACTCGACAACTTTTCGACGCGCTGTGACAAAGATCACTGACGCCATGAGA 366

QY 1731 gaatcgaaggttcttgaatttttgcatgctgtggaacacttgacatacagaagaatgac 1790
 |||||
 Db 367 GAATCAAGGTTCTTGAATTTCAGCATGCGTTGGAACACATTTGGCTTACAGAAATATGAC 426

QY 1791 ttgaagagttcgtgcccagacaatcagctcttaccagcttgagcgaacttgaaggttg 1850
 |||||
 Db 427 TTTGAAGAAATTCGTGCTGACAGCAATCAGCCCTTACCAAGCTTGAAGCTTTGAAGGTGG 486


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Db      602 CAGCAATTTTCCGGTCTGTGTACGACGAAATCTAATCTTGTATGATTCACC 654
RESULT 6
BF520876 622 bp mRNA EST 08-DEC-2000
LOCUS     EST458349 DSIL Medicago truncatula cDNA clone pDSIL-23N23, mRNA
DEFINITION
sequence.
ACCESSION BF520876
VERSION    BF520876.1 GI:11609559
KEYWORDS   EST.
SOURCE     barrel medic.
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
            Medicago.
REFERENCE 1 (bases 1 to 622)
AUTHORS   Fedorova,M., Plesion,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng
            ,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
            Holt,I.E. and Fraser,C.M.
TITLE      ESTs from leaves of Medicago truncatula after inoculation with
            Colletotrichum trifolii
JOURNAL    Unpublished (2000)
COMMENT    Contact: Deborah A. Samac
            Department of Plant Pathology
            University of Minnesota
            495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
            Tel: 612 625 1243
            Fax: 651 649 5058
            Email: debysp@umn.edu
            University of Minnesota name: M278318e
            TIGR sequence name: MTFDA84TK
            More information is available at: http://chrysis.tamu.edu/medicago
            Seq primer: Skmod (CTA gaa CTA gtc gat CC).
            Location/Qualifiers
                1..622
                /organism="Medicago truncatula"
                /cultivar="genotype A17"
                /db_xref="taxon:3880"
                /clone="pDSIL-23N23"
                /clone_1lb="DSIL"
                /tissue_type="Leaves infected with Colletotrichum
                trifolii"
                /dev_stage="cotyledons and primary leaves harvested 5 and
                8 days after inoculation with Colletotrichum trifolii"
                /lab_host="E. coli strain XL0LR"
                /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                XhoI; cDNA was prepared from polyA+ enriched RNA from
                cotyledons and primary leaves harvested 5 and 8 days after
                inoculation with Colletotrichum trifolii. The cDNA was
                directionally ligated into the uni-ZAP XR vector from
                Stratagene and packaged using GigaPack III Gold packaging
                extracts. Plasmids containing cDNA inserts were excised
                from the recombinant lambda-ZAP phage using Ex-Assist
                helper phage and propagated in XL0LR cells. Note: EST may
                be of fungal origin."
BASE COUNT 174 a 114 c 144 g 189 t 1 others
ORIGIN
Query Match 15.3%; Score 363; DB 11; Length 622;
Best local Similarity 74.0%; Pred. No. 5,6e-49;
Matches 455; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
QY 987 atattgacagagcgagcgagatacacagagagagatgcgaagcgatgtgtacagatt 1046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 ATTTAATGAGAGAGGTGAGATACACAGAGAGAACGCCAAGTATTCTTCTACAAATT 61
QY 1047 ttgagcgtaataagctcttcacatccagggggtatgcatgcatgttggaagccagag 1106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 CTGAATGTAGTGGCTTTGTTCATCTCCAGGAGAGTGTTCACGATCTAAACACAGAG 121

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QY 1107 aatttcctttccaaaccagggatgaaatgctcccatgaagtgtatgtattgtgtc 1166
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Db 122 AATTTCTTTTGTCTCAAAAGATGAGAGATCGTGTCTGAAAGTATTATGATTTTGGCTA 181
QY 1167 tctgattcattagaccagagatgaaggcttaatgatatgtgtggaagtcatattgt 1226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 TCTGATTTTGTGTAGCCAGGAGCGCCCTCAATGATATTGTTGATGCTCTATATT 241
QY 1227 gccccagaggttttacacagatcatatagtagtaagagcagacattggagtagtg 1286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 GCACCTGAAAGTGTCCATATATCTTACAGCGTTGAAACACACTTGTGAGATTGGAGTT 301
QY 1287 ataagttacattctgtctctgttcgacgtcggccattctgycgacgaacaagaata 1346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 ATATCGACATATTATTATGTGAGAGTACACCGTTTGGCAGACAGAAATCAGGAATT 361
QY 1347 ttccgattctgttgagagctgatacccaactttgatgattccacgtgacctaatca 1406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 TTCCGGTCTGTGTACAGCAGCAAAATCCAACTTGATGATATTCACCTTGGCCATCAATT 421
QY 1407 gctgaagctgaagatttctgtaagagattctgaacaagaattaccgcaagaatgacc 1466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 CCGAAGCTAAGACTTCTGTGAAGAGACTTTTGACAGAGACACACAGAAAGATGACT 481
QY 1467 gctgtcaagcactgtacatccctgtgttgagatgaacaagagcagatcccgctgac 1526
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 GCGGTCTAAGCTTTATCTCATCCCATGTTGAGAGATGAAAAAATGTCGTTCTTATGAT 541
QY 1527 ataactcttcagatgaatgaagaatcctccgcgtacaccttaagcggttgca 1586
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 ATTTGATTTTACAGTAGTCAATATGATGCGCCCTCGCATTTGAACGTCGCGCA 601
QY 1587 ttaagagcactatcccaagc 1606
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Db 602 CTGAAGGCTCTCTCAAAAGC 621

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RESULT 7
BG592840 758 bp mRNA EST 12-APR-2001
LOCUS     EST491518 cSTS Solanum tuberosum cDNA clone cSTS2F17 5' sequence.
DEFINITION
mRNA sequence.
ACCESSION BG592840
VERSION    BG592840.1 GI:13610980
KEYWORDS   EST.
SOURCE     potato.
ORGANISM   Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 758)
AUTHORS   van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chienlingo,A.,
            Bougri,O., Buell,C.R., Koenning,C., Tanksley,S. and Baker,B.
TITLE      Generations of ESTs from sprouting potato eyes
JOURNAL    Unpublished (2000)
COMMENT    Contact: Cathy Rinning
            The Institute for Genomic Research
            For clone info: please contact Research Genetics, Libraries
            Division tel 1-800-711-6195, email cdna@esgen.com
            Seq primer: M13F-R.
            Location/Qualifiers
                1..758
                /organism="Solanum tuberosum"
                /cultivar="Kennebec"
                /db_xref="taxon:4113"
                /clone="cSTS2F17"
                /clone_1lb="cSTS"
                /tissue_type="sprouting eyes from tubers"
                /dev_stage="12-14 weeks post harvest"
                /lab_host="SOLR"
                /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                XhoI; Various sizes of sprouting eyes (2mm to 15mm) were

```


| | | | |
|-----------------------|--|---|-------------|
| OY | 1291 | cgtacat | 1297 |
| | | | |
| DB | 549 | CTTATAT | 555 |
| <hr/> | | | |
| RESULT | 9 | | |
| LOCUS | BG351862 | | |
| DEFINITION | 135B07 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA sequence. | EST | 01-MAR-2001 |
| ACCESSION | BG351862 | | |
| VERSION | BG351862.1 | | |
| KEYWORDS | GI:13180604 | | |
| SOURCE | EST. | | |
| ORGANISM | potato. Solanum tuberosum | | |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. | | |
| AUTHORS | 1 (bases 1 to 743) | | |
| TITLE | Nilsen,K.L., Crookshanks,M., Emmersen,J. and Welinder,K.G. | | |
| JOURNAL | EST-sequencing of mature potato tuber (Var. Kuras) | | |
| COMMENT | Unpublished (2000) Contact: Karen G. Welinder Institut for bioteknologi Aalborg Universitet Soengardaerholmsvej 49, 9000 Aalborg, Denmark Tel.: +45 96358467 Fax: +45 98141808 Email: kgyw@bio.auc.dk Sequenced from the 5' end. High quality sequence stop: 743 POLYA-No. | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..743 /organism="Solanum tuberosum" /cultivar="Field grown Kuras" /db_xref="taxon:4113" /clone_id="Mature tuber lambda ZAP" /tissue_type="Tuber" /note="Vector: Lambda ZAP" | | |
| BASE COUNT | 198 a 138 c 175 g 232 t | | |
| ORIGIN | | | |
| Query Match | 14.9%; Score 353.8; DB 11; Length 743; | | |
| Best Local Similarity | 69.0%; Pred. No. 1.6e-47; | | |
| Matches | 500; Conservative 0; Mismatches 222; Indels 3; Gaps 1; | | |
| OY | 942 | tacattcgcataaggaattatctgtagggaggagaagtgtcgtagagacaatatlagccagaagc | 1001 |
| | | | |
| DB | 6 | TATAATAGCATCGAATTGTATGTAAAGGAGAGAAATTCGTGGACCGATATCTTCCCAAGGGCT | 65 |
| OY | 1002 | ggagatcacacagagaaagatgccaaaacgatgtgttgtaacagatttgagagttgagctagacc | 1061 |
| | | | |
| DB | 66 | GGAAGAATFACCTCGGAGAGACGATGCCAAAGCTGCATGTCGTAACCTTTAGAGCTGTGCTG | 125 |
| OY | 1062 | tcttcgtcatcttcaggaggtagtcgcatcgtgatttgaaagccagagaattcccttcacaa | 1121 |
| | | | |
| DB | 126 | TACTGTCAATCTTCAAGGGGTTGTTCATGCGCACCTAAAGCCTGAGAATTTCTTTTCGTT | 185 |
| OY | 1122 | accagagatgaaaatgctcccacatgaagtgtattgttgtctctcgtcattcaattcatta | 1181 |
| | | | |
| DB | 186 | TCTTAGGATGAAACTCTTCCTTTAAAGGCATGTGACTTTGGCTTCCGATTATGTAAAA | 245 |
| OY | 1182 | ccaagatgaaggcttaatgatalctgttggaagtgatatactatgttgcaccagaaggtlta | 1241 |
| | | | |
| DB | 246 | CCAGATGAAAAGCTTAATGATATATTGTGCGAAGTGACATACTATGTTGCACCTGAGGTTTTG | 305 |
| OY | 1242 | cacagatcataagratatggaagcaaacatttggaatgatagtggtcataacgtaactctg | 1301 |
| | | | |
| DB | 306 | CATGATCTTATGGAACAAGAACCTACATGTGAGATTGCTGTAATTCATATATTTCTT | 365 |

| | | | |
|-----------------|---|--|------|
| OY | 1302 | cctcgtgacgcagtcggccatcttggcagcaagaatacaggatatctcgatctggttg | 1361 |
| Db | 366 | CTTTGTGGAAAGCAGACCTTTTCTGGCGCCGACAGAAGTCGTGATATTTRAGGCCATCTGTG | 425 |
| OY | 1362 | agaagctgatcccacaactttgatgatltcacccgttgccctacagtatcagctgaagctaagat | 1421 |
| Db | 426 | AAAACGTATCCAACCTTTTGACGAATCCCTTG6GCCCTTTGTCTTGATGAGCATGATAGC | 485 |
| OY | 1422 | tcttgtgaagagattcttgaaacaagaattaccgcgaaaagaatgtaaccgctgtgtccaagactg | 1481 |
| Db | 486 | TTTTGTAAAAAAGATTGCTGTAATAAGGATTATCCCAAAAGGCTTAACGCAGCTCAGGCTCTGC | 545 |
| OY | 1482 | acctatcccttggttg---cgagatgacaagaagcagatcccgcttgagacatcctaacttc | 1538 |
| Db | 546 | AGTATCTCTTGTTGGTGGCTGTCTATCATATGACGTGAAMGATTTCTTTGGATATGATACTATAT | 605 |
| OY | 1539 | agattaataagaacatcatccctccgcgtataaccctcttaaocggttgatcattaagaagcacta | 1598 |
| Db | 606 | AAGCTTTATAAAGCTATATGCTATTTCTTCTCTTAGAAAAACGCTTTTAAGGCTCTTT | 665 |
| OY | 1599 | tccaagcgtttaagayggaagatgaactttgtatclctaaactgcagtttaaacctgctgaa | 1658 |
| Db | 666 | GCTTAAGCAATTGGCTATACCACAACATAGCTTATCTCGATGACAGTTTAACCTATTATAGG | 725 |
| OY | 1659 | cctag 1663 | |
| Db | 726 | CCAAG 730 | |
| RESULT | 10 | | |
| LOCUS | T18715 | | |
| DEFINITION | T18715 491 bp mRNA EST 17-OCT-1996 | | |
| VERSION | 5C04G11..T7 membrane-free polysomes from endosperm Zea mays cDNA | | |
| KEYWORDS | clone 5C04G11 5' end similar to calcium dependent protein kinase, | | |
| SOURCE | mRNA sequence. | | |
| ORGANISM | T18715 | | |
| ACCESSION | T18715.1 GI:485645 | | |
| REFERENCE | EST. | | |
| AUTHORS | Zea mays. Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 491) Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T., Helenjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and Larkin,B. Partial sequencing and mapping of clones from two maize cDNA libraries Plant Mol. Biol. 26, 1085-1101 (1994) | | |
| JOURNAL MEDLINE | 95111093 | | |
| COMMENT | Contact: The Maize cDNA Project | | |
| | Helenjaris TG (primary contact) Dept. of Plant Sciences University of Arizona Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721 ph: 602-6218-746 fax: 602-621-7186 E-mail: helenjars@cit.arizona.edu | | |
| | Chris Baysdorfer Department of Biological Sciences, School of Science California State University, Hayward Hayward, CA 94542 ph: 510-881-3459 fax: 510-727-2035 E-mail: cbaysdore@sl.csuhayward.edu | | |
| | Rob Ferl Interdisciplinary Center for Biotechnology Research DNA Sequencing Core University of Florida | | |

P.O. Box 10695
Gainesville, FL 32611-0695
Ph: 904-392-1928, ext. 301
Fax: 904-392-4072
E-mail: roberthnerwm.nerdc.ufl.edu

Seq primer: 77

FEATURES
source Location/Qualifiers
1..491

/organism="zea mays"
/strain="W64A2"
/db_xref="taxon:4577"
/clone="5C04G11"
/lab_host="DH10B"
/note="Vector: Ziplox; Site.1: SalI; Site.2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo- dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA Pol. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the Ziplox phage vector, excised as plasmids, and then individually analyzed."

BASE COUNT 127 a 98 c 115 g 136 t 15 others
ORIGIN

Query Match 14.2%; Score 337.2; DB 11; Length 491;
Best Local Similarity 86.9%; Pred. No. 8.2e-45;
Matches 385; Conservative 0; Mismatches 56; Indels 2; Gaps 2;

QY 1168 ctgattctatctgaccagatgaaggttaatatgattgttggaagtgcatattatgttg 1227
DB 50 CGGATTTATTTAGACCAAGTGAAGGCTCAATNATATTTGGAGAGTCTTATATGTTG 109
QY 1228 cccagaggtttacacagatcataatgataagagagacatttgagagtaagtgca 1287
DB 110 CTCAGAGGTTCTACANAGATCATACATATGGAAGCAAGACATTTGGAGTATGAGTGT 169
QY 1288 taagtaattctctctgtgtgagtcgagcattctgggcaagacagatcaagaaat 1347
DB 170 TAAAGTACATTCTGCTCTGCGACGTCGACATCTGGCGANGACAGAAATCTGGATNT 229
QY 1348 tccgactcgtgtgagagctgatacccaattgattatccctgtgctcagatcag 1407
DB 230 TCCGCTCGGATTTGAGGCTGATCCNNATTTTAAGATTCACCATGGCTTACGATACGG 289
QY 1408 ctgaagctaaagatttctgaaagattctgaacaagaatla-cgcgaagaatgacc 1466
DB 290 NNGAGGCTAAGAGATTTGTGAAGAGATTTCGAACAAGATTACCCCAAAAGATGACT 349
QY 1467 gctgttaagacactgactcatccttctgttcgagataaacaagcagatcccgctgac 1526
DB 350 GCTGTCCAAAGCACTGACTCACCTTGGTTACGNGATGAACAAGCAAAATTCATTCGAC 409
QY 1527 atactcatctcagattaatgaacaatctcgcgcgtcactcactcttaacgctgca 1586
DB 410 ATACTCATNTTCAGNTTAGTTTACCAATATCTCGTNCCTACTCTTAACGTTTGA 469
QY 1587 ttaagacactatccaagctt 1609
DB 470 TTAAGG-ACCTTCTAAGCTTT 491

RESULT 11
LOCUS BF421980 575 bp mRNA

DEFINITION FM1_11.G09.g1_A003 Floral-Induced Meristem 1 (FM1) Sorghum

ACCESSION BF421980

VERSION BF421980.1 GI:11409871

KEYWORDS EST.
SOURCE Sorghum proplinqum.

ORGANISM

Sorghum proplinqum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE

AUTHORS

Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and Pratt
L.H.

TITLE

An EST database from Sorghum: floral-induced meristems

JOURNAL

Unpublished (2000)

COMMENT

Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805

Email: mpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.

Seq primer: POLYTMX

High quality sequence start: 5

High quality sequence stop: 570

POLYA-No.

FEATURES
source Location/Qualifiers
1..575

/organism="Sorghum proplinqum"
/db_xref="taxon:132711"
/clone="1b-"Floral-Induced Meristem 1 (FM1)"

/note="Organ: Floral-Induced meristems; Vector:
pBluescript II from lambda Zap II; Site.1: XhoI; Site.2:
EcoRI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested. The
library was made from poly-A RNA in the cloning vector
lambda Zap II. Clones to be sequenced were prepared by
mass excision."

BASE COUNT 153 a 119 c 134 g 169 t
ORIGIN

Query Match 14.1%; Score 333.6; DB 11; Length 575;
Best Local Similarity 77.7%; Pred. No. 3e-44;
Matches 432; Conservative 0; Mismatches 114; Indels 10; Gaps 2;

QY 1698 gcaactaagcagatattactgtctgctatgaagaatcgaggcttctgaatttgcatt 1757
DB 1 GCTGTGACAGATATTTAATGATGATGAGAGATCAAGGCTCTTGAGTTTGCAT 60
QY 1758 gctgtgaaccacttgcatacaagaatggaacttgaagagcttctgtccgagcaatc 1817
DB 61 GCGCTGGAACCACTTTCGCTGACGAAGAATGACCTTTGAAGAATTTTGTCTGACGAATC 120
QY 1818 agctcttaccagcttgaagcacttgaagagtgaggagagatgcttgaacaagcttccag 1877
DB 121 AGCCCATACACAGCTCGAGCTTTGGAAGGTGGGAAGAAATTGCTGGAACACTTTTCAG 180
QY 1878 caatttgaacagagagggcaacgagtcatacatcagttgaggaattgacacaggaatnaat 1937
DB 181 CACTTTGAACAAGAGGCAACGAGTTATATCGTTGAGAGACTTGCACAGCAACTTAAT 240
QY 1938 ctgtctcaactcattaccatcgttcaagaactgatacagaagaatccgactgagaagcta 1997
DB 241 CTCGGGCCAATCATTTACATTCGTCGAAGCTGATGACGAAGATCGGACGCAAGCTT 300
QY 1998 aacttctcgggttcaacaattttacatggttcacaataaaggaggtcacaatacaaga 2057
DB 301 AACTTCTTGGGTTTACCAAAATTTTGCATGCTGACAAATCGGGGCTCAAAATTCAMGA 360
QY 2058 cggcattaaagcatttgaanaaagaatgtatcttctctctcttaatttaagcgct 2117
DB 361 CCACACTAANTGTTGCAAAATTTGATTTGATTTAAAGCCTTCATCA----- 413

| QY | 2118 | catltygaccctgattgagtttccctccctcgtctctatacct--ctgtaacatg | 2175 |
|---|--|--|------------------------------------|
| Db | 414 | -ATTATATGAGCCCGATATGCTTATACCCCTGCCTCTCTCTGCGCCCTTCCTTTGG | 472 |
| QY | 2176 | atcattatctgttcgctgcctgcctgctgttgcatacatagttttgtagaata | 2235 |
| Db | 473 | TCAATGACCATTCCTGTTTGATGATGATCCCGGTTTGTCTGCAATAGCTTTTGTAGAGTA | 532 |
| QY | 2236 | catgtaagaatcttt | 2251 |
| Db | 533 | CATGTAAGATCCTGT | 548 |
| RESULT | 12 | | |
| LOCUS | Al1487355 | 653 bp | mRNA |
| DEFINITION | EST245677 | tomato ovary, TAMU | Lycopersicon esculentum cDNA clone |
| ACCESSION | U1487355 | | mRNA sequence. |
| VERSION | U1487355.1 | GI:4382726 | |
| KEYWORDS | EST. | | |
| SOURCE | tomato. | | |
| ORGANISM | Lycopersicon esculentum | | |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; | | |
| AUTHORS | 1 (bases 1 to 653) | | |
| Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Romling,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nieman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksey,S.D. and Giovannoni,J. | | | |
| Generation of ESTs from tomato carpel tissue | | | |
| Unpublished (1999) | | | |
| CONTACT | CUGI | | |
| Clemson University Genomics Institute | | | |
| Clemson University | | | |
| 100 Jordan Hall, Clemson, SC 29634, USA | | | |
| Email: http://www.genome.clemson.edu/orders/index.html . | | | |
| Location/Qualifiers | | | |
| 1..653 | | | |
| /organism="Lycopersicon esculentum" | | | |
| /cultivar="T1496" | | | |
| /db_xref="taxon:4081" | | | |
| /clone="U1487355" | | | |
| /clone_1id="tomato ovary, TAMU" | | | |
| /tissue_type="carpel" | | | |
| /dev_stage="5 days pre-anthesis to 5 days post-anthesis" | | | |
| /lab_host="X11-Blue MRP" | | | |
| /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lambda Zap II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively." | | | |
| BASE COUNT | 197 a | 121 c | 142 g |
| ORIGIN | | | 193 t |
| Query Match | 14.1% | Score 333.6; | DB 10; Length 653; |
| Best Local Similarity | 69.5%; | Pred. No. 2.9e-44; | |
| Matches 453; Conservative 0; | Mismatches 199; | Indels 0; | Gaps 0; |
| QY | 1366 | ctgaccccaacttattgattaccggtgtgctcaagatcatgaagtaagatttg | 1425 |
| Db | 1 | CTGATCTCAATTTTATGAGCATCGCTTGCGCTGACGTGCACAGAGCCACAGATTTTG | 60 |
| QY | 1426 | tgaagagatttcgacaagaattccgcaagaagatgacccgtgttcaagacgactc | 1485 |
| Db | 61 | TGAAAAGGCTTTTGAATTAAGACCATAGGAAGAATGACTCTTCTCAAGCAGCTGACAC | 120 |
| QY | 1486 | atccttggttcgagatgacaagaagcagcatccgcgtgacatactcatcttcagattaa | 1545 |

[illegible]

directionally cloned cDNA in vector Lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

Query Match 14.0%; Score 332; DB 10; Length 653;
Best Local Similarity 69.3%; Pred. No. 5.3e-44;
Matches 452; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

Db 1 CTGATCTTAATTTGAGAGCTCGCTTGGCTGAGTGCAGCGAGCGCAGAGATTTTG 60
Qy 1366 ctgattcccaacttggatgattcaacgctgacctagatcatgagctgaagcttaagatttg 1425
Db 1426 tgaagagaattctgaaagattaccgcaaaagaagacgctgcttcaagacattgact 1485
Db 61 TGAAGAGGCTTTGATTAATTAAGACCATAGAGAGAGATGACTGCTTCTCAAGCAGCTGACTC 120
Qy 1486 atcccttgctgcagatgaaacaaagcagatcccgctgcagatactcatcttcagattaa 1545
Db 121 ATCCATGTTTGAAGAGCTGAAGAAATCCTTTTGACCCCTTAGACATATGTATCTTTAAATTAG 180
Qy 1546 ttaagcaataccctccgcgtacacacctttaaaggttgcatlaaaggaacatccaaag 1605
Db 181 TCAAGTCTTATATCGAATCATACCCCTTGAAGCAGCAGCAGCACTGCTTTCAAAAG 240
Qy 1606 cttaagggagatgaaacttttgatctcaaacgctgaactgaactgaactgaag 1665
Db 241 CATTGACAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
Qy 1666 atgggttctgatactgatacaacttccgacgagcaactaagcagatatttaactgattcta 1725
Db 301 CTGGTTTGTGCTACGTGATTAATTTTGAATGGCAGCTTATGAAGAAACAGCAGCTATGCCA 360
Qy 1726 tgaaggaatcgaaggttcttgaatttgcagtcgcttggaacacattgatacagaagaa 1785
Db 361 TGAAGGAGGCGCAGAGTCTTGACATCATTAATTTGCTGAGAACCATTAATCTTATTAAGCAA 420
Qy 1786 tgaagacttgaagatgcttgcgcgcagcaatcagctccttccagcttgaagcactgtaaa 1845
Db 421 TGGATTTTGAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Qy 1846 gctggaagagatgctgcgacagcttccagcaatttgaacaaaggaagcagcaatca 1905
Db 481 ACTGGGAAACATATTGCTAGAGCGGCTTTCAATTAATTTTGAAGAAAGAAAGAAACCGTCTCA 540
Qy 1906 tctcagttgagaattagacagaagaaatcaacttgcctcaactacttactcatcgtctc 1965
Db 541 TTTCTGTTGAGGAAATTAAGCAGAGAAATGAATTTGGGCGCTACGGCTTATGCTTTCTCA 600
Qy 1966 aagactggaatcagaagaatccgattgcaagtaacttcccggtttaccaa 2017
Db 601 AGGATTGATCAGACCATCCGATAGAGAAATTTGAGTTCTTGGGTATTAACCA 652

RESULT 14

LOCUS AM688043 551 bp mRNA EST 15-JUN-2000
DEFINITION NF003F12ST.1F1000 Developing stem Medicago truncatula cDNA clone
ACCESSION AM688043
VERSION AM688043.1 GI:7562867
KEYWORDS EST.

SOURCE Medicago truncatula

ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE 1 (bases 1 to 551)

AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon

TITLE 'R.A.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
Unpublished (2000)

COMMENT JOURNAL Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 551 Std Error: 0.00
Plate: 003 Row: F Column: 12
Seq primer: TCACACAGGAAACAGCTATGAC.

FEATURES location/Qualifiers

1..551
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/db_xref="taxon:3880"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
intermodal stem segments"

BASE COUNT 173 a 74 c 140 g 164 t

Query Match 13.7%; Score 325.4; DB 10; Length 551;
Best Local Similarity 74.4%; Pred. No. 6.3e-43;
Matches 410; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

Qy 779 gtacaagggagagacccgtccgctcagatgatactccaaagctaaagatgacaggaat 838
Db 1 GTTTAAGGCTCAACAAATGGCTGTCAAGATTTCTTAAGCAAGATGACACAGCAAT 60
Qy 839 atccatgagagatgctgcagaaagaaatlttgaagcgttcaacagggcacaataa 898
Db 61 TGCATTTGAAGATGTGAGAGAGAGGTCMAAATTTGCGAGCTTTGAACGGGACACCA 120
Qy 899 tctcgtcaaatctctatgatacgtgagatggcctcaatgcttcaatgctatgtaatt 958
Db 121 TTTGCTAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Qy 959 atgtgaagggagaaatgtgtgaacagaaatgaacgaagggcgaggaatcaacagaga 1018
Db 181 ATGTGAAGGGGAGAGCTATTAGACATGATCTATCAAGAGAGGAGAAATCTCAGAGA 240
Qy 1019 agatgccaagagatgtgtacagatttgaagcgtatgaagccttgcatacttcaggg 1078
Db 241 TGATGCCAAAGCGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Qy 1079 ggtatgcatcgtgatttgaagccagagaatttcccttcaacacaggaatgaatgc 1138
Db 301 TGTGCTGACAGAGATCTTAAGCCTGAGAAATTTTGTGACACTCAAGAGATGAATCTTC 360
Qy 1139 tccatgaagatgattgatttgcctcctcttcaatgaagccagatgaagcgttaa 1198
Db 361 TGAATTTAAAGCTATTAACCTTTGGTGTGAGATTTTGTGACACCAATGAAGGCTTAA 420
Qy 1199 tgatatgttgaagatcattatgctgtcccgagaggtttcaacagacataagat 1258
Db 421 TGATATTGTTGGAAGTGCATATTATGCTGCTCGTGAAGTTCTCCATATGATCTTAAGTAC 480
Qy 1259 ggaagcagacatttgaagatagatgctcaacagatcatcgtcctgctgagcgtgcgc 1318
Db 481 AGAAGCTGAGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy 1319 atcttgagcag 1329
Db 541 ATTTTGGGCTC 551

| RESULT | 15 | LOCUS | AU032386 | 326 bp | mRNA | EST | 20-OCT-1998 |
|-----------------------|---|--|--------------|------------|-----------|---------------|-------------|
| DEFINITION | AU032386 | Rice root | Oryza sativa | CDNA clone | R3979_1A, | mRNA sequence | |
| ACCESSION | AU032386 | | | | | | |
| VERSION | AU032386.1 | GI:3768359 | | | | | |
| KEYWORDS | EST. | | | | | | |
| SOURCE | Oryza sativa. | | | | | | |
| ORGANISM | Oryza sativa. | | | | | | |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza. | | | | | | |
| AUTHORS | 1 (bases 1 to 326) | | | | | | |
| TITLE | Minobe, Y. and Sasaki, T. | | | | | | |
| JOURNAL | Rice CDNA from root | | | | | | |
| COMMENT | Unpublished (1995) | | | | | | |
| | Contact: Takuji Sasaki | | | | | | |
| | National Institute of Agrobiological Resources | | | | | | |
| | Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki | | | | | | |
| | 305-8602, Japan | | | | | | |
| | Tel: 81-298-38-7441 | | | | | | |
| | Fax: 81-298-38-7468 | | | | | | |
| | Email: tassaki@agr.affrc.go.jp, URL: http://rpg.dna.affrc.go.jp/PROJECT="RGP" | | | | | | |
| FEATURES | Location/Qualifiers | | | | | | |
| source | 1..326 | | | | | | |
| | /organism="Oryza sativa" | | | | | | |
| | /strain="Nipponbare, sub-species Japonica" | | | | | | |
| | /db_xref="taxon:4530" | | | | | | |
| | /clone="R3979_1A" | | | | | | |
| | /clone_1lb="Rice root" | | | | | | |
| | /note="Prepared from seedling root." | | | | | | |
| BASE COUNT | 93 a 73 c 73 g 86 t | | | | | | |
| ORIGIN | | | | | | | |
| | 1 others | | | | | | |
| Query Match | 13.6%; Score 321.8; DB 10; Length 326; | | | | | | |
| Best Local Similarity | 99.1%; Pred. No. 2,7e+42; | | | | | | |
| Matches | 323; Conservative 0; Mismatches 3; Indels 0; Gaps 0 | | | | | | |
| OY | 1266 | gacattgagatagatagatgacaaacgtacattctgctctgtgcaagtcgcgcattctgg | 1325 | | | | |
| DB | 1 | GACATTTTGAGATATAGGTGTGATTAACGATTCGCTGCTGTGGCAGTGGCGCATTCG | 60 | | | | |
| OY | 1326 | gcacgaacagatcgggaatatctcgatctggttgagagcgcgattcccaacttgatgat | 1385 | | | | |
| DB | 61 | GCACCAACAGATTCAGGATATTCGATCTGTTGAGAGCGATGCCAACTTTGATGAT | 120 | | | | |
| OY | 1386 | tcaacgtgagcctacagatctcaagctaaagatttgtagaagatcttctgaacaaa | 1445 | | | | |
| DB | 121 | TCACGTGGCTTCACGTATCAGCTGACGTAAAGATTGTTGTAAGAGATTTCTGACACAA | 180 | | | | |
| OY | 1446 | gattaccgcaaaagaatgaccgctgttcaagacactgacatcatcctgtgtcgagatgaa | 1505 | | | | |
| DB | 181 | GATTACCGCAAAAGAATGACCGCTGTTCAAGCAGTGCATCATCTTGTTGGAGATGAA | 240 | | | | |
| OY | 1506 | caaaagcagatccgcctgagacatactcatcttcagattaatgaagaatacctcgcgct | 1565 | | | | |
| DB | 241 | CAAAAGCAGATCCCGCTGACATCTTCAGATTAATTAAGCAATACTCCCGCGCT | 300 | | | | |
| OY | 1566 | acaactctaaacggttgcattaa | 1591 | | | | |
| DB | 301 | ACACCTTTAAACGGGTTNGCATTTAA | 326 | | | | |

Search completed: May 2, 2002, 06:25:09
Job time: 6414 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2002, 06:30:06 ; Search time 80.44 Seconds

(Without alignments)
573.690 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260
Sequence: 1 MGCCYKGAGSRTADEGGV.....LGFTKLHGVTIRCSNTRRH 623

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|----------------------|
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| 2 | 1948.5 | 59.8 | 594 | 21 | Arabidopsis thaliana |
| 3 | 1801.5 | 55.3 | 502 | 21 | Arabidopsis thaliana |
| 4 | 1790 | 54.9 | 504 | 21 | Arabidopsis thaliana |
| 5 | 1596 | 49.0 | 428 | 21 | Arabidopsis thaliana |
| 6 | 1534 | 47.1 | 414 | 21 | Arabidopsis thaliana |
| 7 | 1377 | 42.2 | 368 | 21 | Arabidopsis thaliana |
| 8 | 1065.5 | 32.7 | 523 | 21 | Arabidopsis thaliana |
| 9 | 967 | 29.7 | 426 | 21 | Arabidopsis thaliana |
| 10 | 934 | 28.7 | 265 | 21 | Arabidopsis thaliana |
| 11 | 908.5 | 27.9 | 463 | 21 | Arabidopsis thaliana |

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| 14 | 868.5 | 26.6 | 459 | 21 | Arabidopsis thaliana |
| 15 | 855.5 | 26.2 | 856 | 21 | Arabidopsis thaliana |
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| 17 | 855.5 | 26.2 | 1017 | 21 | Arabidopsis thaliana |
| 18 | 852.5 | 26.2 | 538 | 21 | Arabidopsis thaliana |
| 19 | 847 | 26.0 | 384 | 21 | Arabidopsis thaliana |
| 20 | 824.5 | 25.3 | 501 | 21 | Arabidopsis thaliana |
| 21 | 816.5 | 25.0 | 483 | 21 | Arabidopsis thaliana |
| 22 | 816.5 | 25.0 | 556 | 21 | Arabidopsis thaliana |
| 23 | 808 | 24.8 | 512 | 20 | Arabidopsis thaliana |
| 24 | 788 | 24.2 | 404 | 21 | Arabidopsis thaliana |
| 25 | 764 | 23.4 | 226 | 21 | Arabidopsis thaliana |
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| 33 | 697 | 21.4 | 274 | 19 | Arabidopsis thaliana |
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| 36 | 524.5 | 16.1 | 307 | 20 | Arabidopsis thaliana |
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| 40 | 509.5 | 15.6 | 355 | 22 | Arabidopsis thaliana |
| 41 | 509.5 | 15.6 | 357 | 22 | Arabidopsis thaliana |
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ALIGNMENTS

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| ID | AAAGS3883 standard; Protein; 594 AA. |
| XX | |
| AC | AAAGS3883; |
| XX | |
| DT | 18-OCT-2000 (first entry) |
| DE | Arabidopsis thaliana protein fragment SEQ ID NO: 68643. |
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| KW | Protein identification; signal transduction pathway; metabolic pathway; |
| KW | hybridisation assay; genetic mapping; gene expression control; promoter; |
| KW | termination sequence. |
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| OS | Arabidopsis thaliana. |
| PN | EP1033405-A2. |
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| PD | 06-SEP-2000. |
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| PF | 25-FEB-2000; 2000EP-0301439. |
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Query Match 55.3%; Score 1801.5; DB 21; length 502;
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| OY | 236 | LKFYDACEDELNVYIMELCEGGELLDRILANGRYTEDAKAIYQIIISVAFCHIQ | 295 |
| DB | 114 | mvkfydvfedsdvnfvymelceggellldslargrypeaseekrlvlqvilsataffhlg | 173 |
| OY | 296 | VVHRDLKPENFLFTTRDENPMKLIDGLSDFTFRPDERLNDYGSAIVYAPVLRHYSM | 355 |
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PN EP1033405-A2.
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 PR 31-AUG-1999; 990S-0151338.
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| PR | 05-OCT-1999; | 99US-0157753. |
| PR | 06-OCT-1999; | 99US-0157865. |
| PR | 07-OCT-1999; | 99US-0158029. |
| PR | 08-OCT-1999; | 99US-0158232. |
| PR | 12-OCT-1999; | 99US-0158369. |
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| PR | 21-OCT-1999; | 99US-0160815. |
| PR | 22-OCT-1999; | 99US-0160980. |
| PR | 22-OCT-1999; | 99US-0160981. |
| PR | 22-OCT-1999; | 99US-0160989. |
| PR | 25-OCT-1999; | 99US-0161404. |
| PR | 25-OCT-1999; | 99US-0161405. |
| PR | 25-OCT-1999; | 99US-0161406. |
| PR | 26-OCT-1999; | 99US-0161359. |
| PR | 26-OCT-1999; | 99US-0161360. |
| PR | 26-OCT-1999; | 99US-0161361. |
| PR | 28-OCT-1999; | 99US-0161920. |
| PR | 28-OCT-1999; | 99US-0161992. |
| PR | 28-OCT-1999; | 99US-0161993. |
| PR | 29-OCT-1999; | 99US-0162142. |

| Query Match | 54.9% | Score 1790: | DB 21: | Length 504: |
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| Best Local Similarity | 67.7% | Pred. No. 11e-131: | | |
| Matches 344: | Conservative 73: | Mismatches 81: | Indels 10: | Gaps 4: |
| QY 117 | ATLAKRLGCG-KPKKEGTPE--EGGVAGAGCGGGAGDAGETRPRLDKTGFSGKNGAKYE | 173 | | |
| Db 2 | aalrrrrgarpqrdepredpsedvvdhngdsagg-----erldknlgfgrknegkye | 54 | | |
| QY 174 | LCKEVRGNHFGHTGSAVYKKGEGYKQOYAVKTIKAAKTTAISIEDVREVKITRLASGH | 233 | | |
| Db 55 | lqkevgtrghfhtcwaakakgmkmqyavakliskakmtstlsdvtrevvllkalsgh | 114 | | |
| QY 234 | NNLVKFDYACSDGLNVYIVMEICEGEGELDLRLARGKRTEDAKAIIVQILSVAFCL | 293 | | |
| Db 115 | rhmwkfyvnyvedadnrvfvmelceggelldrlarggyrpvedarrllvqlisacafhl | 174 | | |
| QY 294 | QGVVNRDLKRENFLETTDENAPMKLLDFGSLDTRPERDLNDIVGSAVYVAEVLHRSY | 353 | | |
| Db 175 | qgvvhrdlkpenflfstrnedal1kv1dfigtsdftrgqrlndvvasyuaeverlhtsy | 234 | | |
| QY 354 | SMEDADWISIGVITITLLCGSRPFMARSGSGFRSLYRDAPNDSDSPWTVSAEAKDFYKR | 413 | | |
| Db 235 | steadmasyt1sylvlll1ogsrtpfygrtsesalfrcvllranpntedmpwpslptackfvr | 294 | | |
| QY 414 | FLNKDYRKRMATVQALTHPMLRDQORLPDLILFRLTKQYLRATPMLRLAKALSKYLR | 473 | | |
| Db 295 | llnkhdkrtmaeqalanhprlrdemngllldfsvykvllksyltraepfrfrrsalkkelsk1p | 354 | | |
| QY 474 | EDELHYLKLQKLELRPRGQFVSLDNFRALRLRYLTDANKESVLEFLALDEPLATRRDF | 533 | | |
| Db 355 | deeeivllkagqtmlldpkkg1slncfhtalcrtyattdammesr1pdl1ntmp1akklidf | 414 | | |

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PR 28-JUN-1999; 99US-0140823.
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PR 30-JUN-1999; 99US-0141287.
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PR 02-JUL-1999; 99US-0142055.
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PR 23-JUL-1999; 99US-0145145.
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PR 26-JUL-1999; 99US-0145276.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149920.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151080.
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PR 07-SEP-1999; 99US-0152363.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match

49.0%; Score 1596; DB 21; Length 428;

Best Local Similarity 70.1%; Pred. No. 1.3e-116;

Matches 298; Conservative 68; Mismatches 59; Indels 0; Gaps 0;

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Db 2 kngtvavkikskamtslistedvrevkiklksghnmvkfydyedadvivmeic 61

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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
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PR 06-AUG-1999; 99US-0147303.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 47.1%; Score 1534; DB 21; Length 414;
Best Local Similarity 69.6%; Pred. No. 9.1e-112;
Matches 286; Conservative 64; Mismatches 61; Indels 0; Gaps 0;

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Db 1 mtsalsiedvrevkllkalsghnmvkvfydvfedsdnfvvmelceggelllsilarg 60
OY 271 RYTEDAKAIYVQILSVAFCHLOGVVRHDLKRPENLFTTRDENAPMKLIDFGISDFIRP 330
||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 rypeaeakrllivqlisatalfhlgvvrhldkpenflitsknedavlkvidfglsdyarf 120
OY 331 DERINDIVGSAVYVAPEVLHRSYSWEADIVGIVTYTILCGSRPFMAFTSGIFRSVLR 390
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AC AAG48297;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60975.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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XX 06-SEP-2000.
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RESULT 9
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XX AAG10102;
AC AAG10102;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 8290.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX Arabidopsis thaliana.
OS
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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KW termination sequence.
OS Arabidopsis thaliana.
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Query Match

27.7%; Score 903.5; DB 21; Length 542;

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| OY | 154 | TERPLDKTFGFSKNGAKYEIAGEVGRGHFGHTCSAVVKKGEYKQOTAAVKITAKAKMTT | 213 |
| Db | 80 | Igrpmeev-----rrtyefelgrejlgqfgytlylvtketk---qyvacskisprtlrvh | 129 |
| OY | 214 | AISTEDVAREVKILIALSGHNHLVFAYDACEOGLNVAITYMEICEGGEILDRIARGBRYT | 273 |
| Db | 130 | kddledvrtrevgllshlnhsghnrlvalkgayedrhsvnlimeiceggeldrilisk-qlys | 188 |
| OY | 274 | EEDAKAIVVOILSVYAFNLHOGVVRDDIKPENFLFTTRDENAPMKLLIDFGLSDFTRPDR | 333 |
| Db | 189 | eraaadlcrgmwvmvhschsmgymbrdlkpenflfIsksdensprlkatdglsvffkpgdk | 248 |
| OY | 334 | LNDIVGSAYIVAPEVLNHSYSMEADIMSIGVTYYILLGSRPFPMARTESGIFRSYIRADP | 393 |
| Db | 249 | fkdilvsayayavepElkrnygspeadlsagavlylllsgvpffwgeneptlfdaal19ql | 308 |
| OY | 394 | NPDDSFWPTVSSEADFPFKRPLNKCYRRKMTPVQAULTHPWMBD--EQQRIPDLIIIRLI | 451 |
| Db | 309 | dtsadwpalsogadldylvrkmikypokdltlaeavlhpwrldedgaadkpldnaa1srzm | 368 |
| OY | 452 | KOYLRTALPKRLKLALKALSREDELTYLKLOFKLE--PRDGFSLDNFRALTTRYLTDA | 510 |
| Db | 369 | kqframkhkkmaIkvaenlseeligkcmfkeldcdmgivltleeltg1pk-19sk | 427 |
| OY | 511 | MKESNVLEFLHALPELAYRRMDFEFPCAALISPYOLEALERWEIEAGTAFAQQEPDEGNFY | 570 |
| Db | 428 | IseaelirqlmeaadmdgdsIdylefisatm---Immrter-edhlytafqfidndnsqy | 483 |
| OY | 571 | TSVEELAEELNALPRTNYSIVQDWIKS-----DCKLNLFGLTKFL | 610 |
| Db | 484 | ltime---elelamkkymgdksikeilaevoldrdgkinpyeeIvanmm | 528 |
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| AC | 17-OCT-2000 (first entry) | | |
| XX | Arabidopsis thaliana protein fragment SEQ ID NO: 35234. | | |
| DE | Protein identification; signal transduction pathway; metabolic pathway; | | |
| KW | hybridisation assay; genetic mapping; gene expression control; promoter; | | |
| KW | termination sequence. | | |
| OS | Arabidopsis thaliana. | | |
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| XX | 25-FEB-1999; 99US-0121825. | | |
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